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(54) Title: Src SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME

(57) Abstract

Peptides having general and specific binding affinities for the Src homology region 3 (SH3) domains of proteins are disclosed in the present invention. In particular, SH3 binding peptides have been isolated from three phage-displayed random peptide libraries which had been screened for isolates that bind to bacterial fusion proteins comprising SH3 and glutathione S-transferase (GST). Preferred peptides are disclosed which comprise a core 7-mer sequence (preferably, a consensus motif) and two or more, preferably at least six, additional amino acid residues flanking the core sequence, for a total length of 9, preferably at least 13, amino acid residues and no more than about 45 amino acid residues. Such peptides manifest preferential binding affinities for certain SH3 domains. The preferred peptides exhibit specific binding affinities for the Src-family of proteins. *In vitro* and *in vivo* results are presented which demonstrate the biochemical activity of such peptides.

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**Src SH3 BINDING PEPTIDES AND
METHODS OF ISOLATING AND USING SAME**

1. Field of the Invention

5 The present invention relates to SH3 binding peptides having a broad range of binding specificities. That is, certain members of the SH3 binding peptides disclosed bind with approximately the same facility with SH3 domains derived from different SH3 domain-containing proteins. Other members, in contrast, bind with a much greater degree of affinity for specific SH3 domains. The SH3 binding peptides are obtained from random peptide libraries that are also phage-displayed. Methods are described of obtaining the phage clones that bind to the SH3 domain targets and of determining their relevant nucleotide sequences and consequent primary amino acid sequence of the binding peptides. The resulting SH3 binding proteins are useful in a number of ways, including, but not limited to, providing a method of modulating signal transduction pathways at the cellular level, of modulating oncogenic protein activity or of providing lead compounds for development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction.

2. Background of the Invention

2.1. Src and the SH3 Domain

25 Among a number of proteins involved in eukaryotic cell signaling, there is a common sequence motif called the SH3 domain. It is 50-70 amino acids in length, moderately conserved in primary structure, and can be present from one to several times in a large number of proteins involved in signal transduction and in cytoskeletal proteins.

30 The protein pp60c-src represents a family of at least nine non-receptor protein tyrosine kinases (NR-PTKs). Members of this family share an overall structural organization comprising a

series of catalytic and non-catalytic domains. In Src, a 14-amino-acid myristylation signal resides at the extreme amino-terminus, and is followed by a unique region that is not highly conserved among family members. Following this region are two highly conserved 60- and 100-amino-acid regions, the Src homology (SH) domains 3 and 2, respectively. SH2 and SH3 domains have been shown to play an important role in mediating protein-protein interactions in a variety of signaling pathways. Koch, C.A., et al., in Science (1991) 252:668-74. The carboxy-terminal half of Src contains the PTK catalytic domain, as well as a negative regulatory tyrosine (Y527) near the carboxy terminus. Phosphorylation of this residue (e.g., by Csk) results in the inhibition of PTK activity. Cooper, J.A., et al., in Science (1986) 231:1431-1434. Mutation of Y527->F generates forms of Src with increased PTK and oncogenic activity. Cartwright, C.A., et al., in Cell (1987) 49:83-91; Kmiecik, T.E., et al., in Cell (1987) 49:65-73; and Piwiczna-Worms, H., et al., in Cell (1987) 75-82.

The fact that some mutations which result in increased Src PTK and transforming activity map to the Src SH2 (Seidel-Dugan, C., et al., in Mol. Cell. Biol. (1992) 12:1835-45; and Hirai, H. and Varmus, H.E. in Mol. Cell. Biol. (1990) 10:1307-1318) and SH3 domains (Seidel-Dugan, C., et al., *supra*; Hirai, H. and Varmus, H.E., *supra*; Superti-Furga, G., et al., in Embo. J. (1993) 12:2625-34; and Potts, W.M., et al., in Oncogene Res. (1988) 3:343-355) suggests a negative regulatory role for these domains. That phosphotyrosine residues within specific sequence contexts represent high affinity ligands for SH2 domains suggests a model in which the SH2 domain participates in Y527-mediated inhibition of PTK activity by binding phosphorylated Y527, thereby locking the kinase domain in an inactive configuration. Matsuda, M., Mayer, B.J., et al., in Science (1990) 248:1537-1539. This model is supported by the observation that phosphopeptides corresponding to the carboxy-terminal tail of Src bind active, but not inactive, variants of Src. Roussel, R.R., et al., in

Proc. Natl. Acad. Sci. U S A (1991) 88:10696-700; and Liu, X., et al., in Oncogene (1993) 8:1119-1126.

The mechanism of SH3-mediated inhibition of Src PTK activity remains unclear. There is evidence that pY527-mediated inhibition of Src PTK activity involves the SH3 domain as well as the SH2 domain. Okada, M., Howell, et al., in J. Biol. Chem. (1993) 268:18070-5; Murphy, S.M., et al., in Mol. Cell. Biol. (1993) 13:5290-300; and Superti-Furga, G., et al., *supra*. Although these effects are thought to be a consequence of SH3-mediated protein-protein interactions, precisely how the Src SH3 domain exerts its negative regulatory effect is unclear. Identification of high affinity ligands for the Src SH3 domain could help resolve these issues.

2.2. Protein Tyrosine Kinases and The Immune Response

Src-related tyrosine kinases are expressed in a variety of cell types including those of the immune system (lymphocytes, T cells, B cells, and natural killer cells) and the central nervous system (neural cells, neurons, oligodendrocytes, parts of the cerebellum, and the like). Umemori, H. et al., in Brain Res. Mol. Brain Res. (1992) Dec. 16(3-4):303-310. Their presence in these cells and tissues and their interaction with specific cell surface receptors and immunomodulatory proteins (such as T cell antigen receptor, CD14, CD2, CD4, CD40 or CD45) suggest that these kinases serve an important role in the signalling pathways of not only the central nervous system but of the immune system, as well. See, e.g., Ren, C.L. et al., in J. Exp. Med. (1994) 179(2):673-680 (signal transduction via CD40 involves activation of Lyn kinase); Donovan, J.A. and Koretzky, G.A., in J. Am. Soc. Nephrol. (1993) 4(4):976-985 (CD45, the immune response, and regulation of Lck and Fyn kinases); and Carmo, A.M. et al., in Eur. J. Immunol. (1993) 23(9):2196-2201 (physical association of the cytoplasmic domain of CD2 with p56lck and p59fyn).

For instance, mice with disruptions in their Src-like genes, Hck and Fgr, possess macrophages with impaired phagocytic

activity or exhibit a novel immunodeficiency characterized by an increased susceptibility to infection with *Listeria monocytogenes*. Lowell, C.A. et al., in Genes Dev. (1994) 8(4):387-398. Also, it has been shown that bacterial lipopolysaccharide (LPS) activates CD14-associated p56lyn, p68hck, and p59c-fgr, while inducing the production of lymphokines, such as TNF-alpha, IL-1, IL-6, and IL-8. Inhibition of the protein tyrosine kinases blocks production of TNF-alpha and IL-1.

2.3. SH3 Binding Peptides

As mentioned above, it has long been suspected that SH3 domains are sites of protein-protein interaction, but it has been unclear what SH3 domains actually bind. Efforts to identify ligands for SH3 domains have led to the characterization of a number of SH3-binding proteins, including 3BP1 and 2 (Ren, R., Mayer, et al., in Science (1993) 259:1157-61), SOS (Olivier, J.P., et al., in Cell (1993) 73:179-91; and Rozakis-Adcock, M., et al., in Nature (1993) 363:83-5), p85 PI-3' Kinase (Xingquan, L., et al., in Mol. Cell. Biol. (1993) 13:5225-5232), dynamin (Gout, I., et al., in Cell (1993) 75:25-36), AFAP-110 (Flynn, D.C., et al., in Mol. Cell. Biol. (1993) 13:7892-7900), and CD42 (Barford, E.T., et al., in J. Biol. Chem. (1993) 268:26059-26062). These proteins tend to possess short, proline-rich stretches of amino acids, some of which have been directly implicated in SH3 binding. A variety of consensus sequences have been proposed, although the similarity among proline-rich regions of different SH3-binding proteins tends to be fairly low. Also, attempts to build consensus sequences are likely complicated by the incorporation of data from proteins that bind different SH3 domains.

Thus, Cicchetti, P., et al., in Science (1992) 257:803-806, published their work relating to the isolation and sequencing of two naturally-occurring proteins that could be bound in vitro by the SH3 domain of the *abl* oncogene product. These workers found

that SH3 domains bind short, proline-rich regions of such proteins. Subsequently, this same group disclosed further results (Ren, R. et al., *supra*) in which the SH3 binding sites of the SH3 binding proteins were localized to "a nine- or ten-amino acid stretch rich in proline residues." A consensus sequence incorporating the features of the SH3 binding sites of four SH3 binding proteins was proposed: XPXXPPPYXP (SEQ ID NO:1), wherein X indicates a position in the amino acid sequence which is not conserved among the four SH3 binding proteins, P represents proline, and Y indicates a hydrophobic amino acid residue, such as P or L.

The screening of complex random peptide libraries has been used to identify peptide epitopes for monoclonal (Scott, J.K. and Smith, G.P., in Science (1990) 249:386-390) and polyclonal (Kay, B.K., et al., in Gene (1993) 128:59-65) antibodies, as well as peptide ligands for a variety of proteins, including streptavidin (Devlin, J.J., et al., in Science (1990) 249:404-406; and Lam, K., et al., in Nature (1991) 354:82-84), the endoplasmic reticulum chaperone BiP (Blond-Elguindi, S., et al., in Cell (1993) 75:717-728), and CaM (Dedman, J.R., et al., in J. Biol. Chem. (1993) 268:23025-23030).

Recently, Chen, J.K. et al., in J. Am. Chem. Soc. (1993) 115:12591-12592, described ligands for the SH3 domain of phosphatidylinositol 3-kinase (PI-3' Kinase) which were isolated from a biased combinatorial library. A "biased" library is to be distinguished from a "random" library in that the amino acid residue at certain positions of the synthetic peptide are fixed, i.e., not allowed to vary in a random fashion. Indeed, as stated by these research workers, screening of a "random" combinatorial library failed to yield suitable ligands for a PI-3' Kinase SH3 domain probe. The binding affinities of these unsuitable ligands was described as weak, >100 μ M, based on dissociation constants measured by the Biosensor System (BIAcore).

More recently, Yu, et al. (Yu, H., et al., in Cell (1994) 76:933-945) used a "biased" synthetic peptide library of the form XXXPPXPXX (SEQ ID NO:2), wherein X represents any amino acid other than cysteine, to identify a series of peptides which bind the Src and PI-3' Kinase SH3 domains. The bias was accomplished by fixing the proline residues at the specific amino acid positions indicated for the "random" peptide. As stated previously, without this bias, the technique disclosed fails to identify any SH3 domain-binding peptides.

A consensus sequence, based on 13 binding peptides was suggested: RXLPPRPXX (SEQ ID NO:3), where X tends to be a basic residue (like R, K or H). The binding affinities of several SH3 binding peptides were disclosed as ranging from 8.7 to 30 μ M. A "composite" peptide, RKLPPRPRR (SEQ ID NO:4), was reported to have a binding affinity of 7.6 μ M. This value compares favorably to the binding affinity of the peptide, VPPPVPPIRR (SEQ ID NO:5), to the N-terminal SH3 domain of Grb2. See, Kraulis, P.J. J. Appl. Crystallogr. (1991) 24:946. Recognizing the limitations of their technique, Chen and co-workers, *supra*, stated that their results "illustrate the utility of biased combinatorial libraries for ligand discovery in systems where there is some general knowledge of the ligand-binding characteristics of the receptor" (emphasis added).

Yu and co-workers, *supra*, further described an SH3 binding site consensus sequence, XpØPpXP (SEQ ID NO:6), wherein X represents non-conserved residues, Ø represents hydrophobic residues, P is proline, and p represents residues that tend to be proline. A consensus motif of RXLPPRPXX (SEQ ID NO:7), where X represents any amino acid other than cysteine, was proposed for ligands of PI-3' Kinase SH3 domain. A consensus motif of RXLPPLPRØ (SEQ ID NO:8), where Ø represents hydrophobic residues, was proposed for ligands of Src SH3 domain. Still, the dissociation constants reported for the 9-mer peptides ranged only from about 8-70 μ M and selectivity between one type of SH3

domain and another was relatively poor, the K_D s differing by only about a factor of four.

Hence, there remains a need to develop techniques for the identification of Src SH3 binding peptides which do not rely on such "biased" combinatorial peptide libraries that are limited to a partially predetermined set of amino acid sequences. Indeed, the isolation of SH3 binding peptides from a "random" peptide library has not been achieved successfully before now.

Furthermore, particular peptides having much greater binding affinities, whether general or more selective binding for specific SH3 domains, remain to be identified. Binding peptides specific for particular SH3 domains are useful, for example, in modulating the activity of a particular SH3 domain-containing protein, while leaving others bearing an SH3 domain unaffected. Still, the more promiscuous general binding peptides are useful for the modulation of a broad spectrum of SH3 domain-containing proteins.

The present invention relates to such SH3 binding peptides, methods for their identification, and compositions comprising same. In particular, peptides comprising particular sequences of amino acid residues are disclosed which were isolated from random peptide libraries. In the present invention, clones were isolated from a phage-displayed random peptide library which exhibited strong binding affinities for SH3 domain-containing protein targets. Some of these protein targets, include Abl, Src, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, and p85 PI-3' Kinase. From the nucleotide sequence of the binding phage, the amino acid sequence of the peptide inserts has been deduced. Synthetic peptides having the desired amino acid sequences are shown to bind the SH3 domain of the target proteins. In particular, synthetic peptides combining a core consensus sequence and additional amino acid residues flanking the core sequence are especially effective at binding to particular target protein SH3 domains. The SH3 binding peptides disclosed herein can be utilized in a number of ways, including the potential modulation

of oncogenic protein activity in vivo. These peptides also serve as useful leads in the production of peptidomimetic drugs that modulate a large class of proteins involved in signal transduction pathways and oncogenesis.

5 3. Summary of the Invention

Accordingly, three phage-displayed random peptide libraries were screened for isolates that bind to bacterial fusion proteins consisting of the Src homology region 3 (SH3) and glutathione S-transferase (GST). DNA sequencing of the isolates
10 showed that they contained sequences that resemble the consensus motif, RPLPPLP (SEQ ID NO:9), within their 8, 22, or 36 amino acid long random regions. When peptides were synthesized corresponding to the pIII inserts of the SH3-binding phage, they bound to the GST fusions of the SH3 domains of Src and the Src-
15 related proteins, such as Yes, but not of Grb2, Crk, Abl, or PLC γ 1. The synthesized peptides bind quite well to the Src SH3 domain and act as potent competitors of natural Src SH3 interactions in cell lysates. For instance, these peptides can compete with radiolabelled proteins from cell lysates in binding
20 to immobilized Src-GST, with an apparent IC₅₀ of 1-10 μ M. When a peptide, bearing the consensus sequence RPLPPLP (SEQ ID NO:9) was injected into *Xenopus laevis* oocytes, it accelerated the rate of progesterone-induced maturation. These results demonstrate the utility of phage-displayed random peptide libraries in
25 identifying SH3-binding peptide sequences and that such identified peptides exhibit both in vivo and in vitro biological activity.

Thus, it is an object of the present invention to provide peptides having at least nine and up to forty-five amino acid
30 residues, including an amino acid sequence of the formula, R-2-L-P-5-6-P-8-9 (SEQ ID NO:10), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 2 represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, 8

represents any amino acid residue except cysteine, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src, provided that said peptide is not R-P-L-P-P-L-P-T-S (SEQ ID NO:11). In a particular embodiment of the present invention, the peptides also exhibit a binding affinity for the SH3 domain of Src-related proteins, including Yes, Fyn, Lyn, Lck, Hck and Fgr.

The present invention also contemplates SH3 domain-binding peptides that further comprise a C-terminal-flanking amino acid sequence of the formula 10, 10-11, 10-11-12, 10-11-12-13, (SEQ ID NO:12) or 10-11-12-13-14 (SEQ ID NO:13), in which each number represents any amino acid residue except cysteine, such that 10 is bound to 9 by a peptide bond. Furthermore, peptides are also provided which further comprise an N-terminal-flanking amino acid sequence of the formula 1', 2'-1', 3'-2'-1' or 4'-3'-2'-1' (SEQ ID NO:14) in which each number represents any amino acid residue except cysteine, such that 1' is bound to R by a peptide bond.

Thus, in a particular embodiment, a peptide is disclosed having at least thirteen and up to forty-five amino acid residues, including an amino acid sequence of the formula, 3'-2'-1'-R-2-L-P-5-6-P-8-9-10 (SEQ ID NO:15), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 3', 2', 1', 2, 8, and 10 each represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src.

The present invention also seeks to provide new consensus sequences or motifs that reflect variations in SH3 domain binding selectivities or specificities. The present invention also contemplates conjugates of the SH3 binding peptides and a second molecule or chemical moiety. This second molecule may be any

desired substance whose delivery to the region of the SH3 domain of a particular protein (or cell containing the protein) is sought. Possible target cells include, but are not limited to, neural cells, immune cells (e.g., T cells, B cells, natural
5 killer cells, and the like), osteoclasts, platelets, epidermal cells, and the like, which cells express Src, Src-related proteins, and potentially, other SH3 domain-containing proteins. In this manner, the modulation of the biological activity of proteins bearing an SH3 domain can be accomplished.

10 Other methods and compositions consistent with the objectives of the present invention are likewise disclosed. In particular, a method is disclosed of modulating the activity of Src or Src-related proteins comprising administering a composition comprising an effective amount of a peptide of the
15 present invention and a carrier, preferably a pharmaceutically acceptable carrier. In a specific embodiment, the contemplated method results in the inhibition of the activity of Src or Src-related proteins. Alternatively, the method is effective to activate Src or Src-related proteins.

20 In yet another embodiment, a method is disclosed of identifying a peptide having a region that binds to an SH3 domain comprising: (a) providing an immobilized target protein comprising an SH3 domain; (b) incubating the immobilized target protein with an aliquot taken from a random peptide library; (c)
25 washing unbound library peptides from the immobilized target protein; (d) recovering the peptide bound to the immobilized target protein; and (e) determining the primary sequence of the SH3 domain-binding peptide.

Moreover, a method is disclosed of imaging cells, tissues,
30 and organs in which Src or Src-related proteins are expressed, which comprises administering an effective amount of a composition comprising an SH3 domain-binding peptide conjugated to detectable label or an imaging agent.

Other objectives of the present invention will become
35 apparent to one of ordinary skill in the art after consideration

of the above disclosure and the following detailed description of the preferred embodiments.

4. Brief Description of the Figures

FIG. 1 illustrates a scheme for the generation of a random 36 amino acid peptide library (TSAR-9; e.g., SEQ ID NO:16). Oligonucleotides were synthesized (SEQ ID NOS:17-18), converted into double-stranded DNA, cleaved with restriction enzymes (SEQ ID NOS:19-20), and cloned into the M13 vector, m663. The random peptide region encoded by the oligonucleotides is shown in the box (SEQ ID NO:16) and is situated at the N-terminus of mature protein III (SEQ ID NO:21).

FIG. 2 illustrates a scheme for the generation of a random 22 amino acid peptide library (TSAR-12; e.g., SEQ ID NO:23). Oligonucleotides were synthesized (SEQ ID NOS:24-25), converted into double-stranded DNA, cleaved with restriction enzymes (SEQ ID NOS:26-27), and cloned into the M13 vector, m663. The random peptide region encoded by the oligonucleotides is shown in the box (SEQ ID NO:23) and is situated at the N-terminus of mature protein III (SEQ ID NO:28).

FIG. 3 illustrates a scheme for the generation of a random 8 amino acid peptide library (R8C; SEQ ID NO:30). Oligonucleotides were synthesized (SEQ ID NOS:31-32), converted into double-stranded DNA, cleaved with restriction enzymes (SEQ ID NOS:33-34), and cloned into the M13 vector, m663. The random peptide region (SEQ ID NO:30) is flanked by cysteine residues and is situated at the N-terminus of mature protein III (SEQ ID NO:35).

FIG. 4 illustrates the possible origin of one class of double-insert R8C recombinants (e.g., encoding SEQ ID NO:36). Double-stranded oligonucleotides (e.g., SEQ ID NO:37) may have ligated in a head-to-head fashion at the Xba I site prior to cloning in the Xho I- Xba I cleaved M13 vector.

FIG. 5 shows a list of random peptide recombinants (SEQ ID NOS:38-61 and 106) isolated by the method of the present invention and the displayed peptide sequence. The amino acid

sequences are aligned to highlight the core sequences. The flanking sequences are shown to the N-terminal and C-terminal ends of the core sequence.

FIG. 6 graphically illustrates the relative binding
5 affinities of selected phage clones for various SH3 domains. The results indicate that certain amino acid sequences provide generic SH3 domain binding, while others can provide greater selectivity for the SH3 domain of Src. Still other clones exhibit Src SH3 domain preferential binding.

10 FIG. 7 shows the binding of synthetic peptides (SEQ ID NOS:9 and 62-70) representing Src SH3-selected phage inserts to Src SH3-GST fusion target (shaded columns) over background GST binding (unshaded columns) relative to the core peptide RPLPPLP (SEQ ID NO:9) and proline-rich peptide segments derived from
15 naturally occurring proteins. Bound biotinylated peptide was detected with streptavidin-alkaline phosphatase ELISA. Each point was performed in triplicate; average absorbance at 405 nm is presented. Error bars represent SD.

FIG. 8 illustrates the relative specificity of selected
20 peptides (SEQ ID NOS:9 and 62-70) for SH3 domains derived from different proteins. In particular, the binding affinities of the peptides for the SH3 domains of the following protein fusion targets were tested: Src SH3-GST, Yes SH3-GST, Grb2-GST, Crk SH3-GST, Abl SH3-GST, PLC γ 1 SH2SH3-GST. Bound biotinylated peptide
25 was detected with streptavidin-alkaline phosphatase. Each point was performed in triplicate; values are average signal (absorbance at 405 nm) above GST background, with error bars representing standard deviation. Hatched bars indicate saturation of the ELISA signal.

30 FIG. 9 presents the results of competition experiments in which selected peptides were found to inhibit the binding of proteins from cell lysates to immobilized Src SH3-GST or Abl SH3-GST protein fusion targets.

FIG. 10 presents a graph illustrating the increased rate of
35 progesterone-induced maturation of oocytes injected with an SH3

domain-binding peptide, VLKRPLPIPPVTR (SEQ ID NO:64), of the present invention. Briefly, Stage VI oocytes were prepared and injected as previously described (see, Kay, B.K., in Methods in Cell Biol. (1991) 36:663-669). Oocytes were injected with 40 nL of 100 μ M test peptide or water. After injection, the oocytes were placed in 2 μ g/mL progesterone (Sigma, St. Louis, MO) and scored hourly for germinal vesicle breakdown (GVBD).

FIG. 11 shows the results of fluorescence experiments in which certain peptides, Panel A = VLKRPLPIPPVTR (SEQ ID NO:64), Panel B = GILAPPVPPRNTTR (SEQ ID NO:63), Panel C = RSTPRPLPPLPTTR (SEQ ID NO:67), of the invention were shown to localize within cellular compartments thought to contain Src or Src-related proteins.

FIG. 12 illustrates a scheme for the generation of a biased peptide library. Oligonucleotides were synthesized, converted into double-stranded DNA, cleaved with restriction enzymes XhoI and XbaI, and cloned into the mBAX vector, described further below in the Examples section. The biased peptide region is situated at the N-terminus of mature pIII protein.

FIG. 13 illustrates the peptide sequence encoded in the mBAX vector situated at the N-terminus of mature pIII protein.

5. Detailed Description of the Preferred Embodiments

5.1. General Considerations

The present invention relates to peptides that exhibit a binding affinity for an SH3 domain, which domain has been found to be present in a number of physiologically significant proteins. In particular, peptides are disclosed which exhibit general binding characteristics to the SH3 domains found in a group of proteins, including but not limited to Abl, Src, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, and p85 PI-3' Kinase. Preferred peptides exhibit selective, if not specific, binding affinity for the SH3 domain of Src. As described herein, the peptides of the present invention include a core sequence, preferably a consensus sequence, and additional amino acid

residues that flank the core sequence. These peptides, including the methods for their identification, are described in greater detail, below.

Thus, in a specific embodiment of the invention, peptides
5 are provided which have at least nine and up to about forty-five amino acid residues, including an amino acid sequence resembling the formula,

R-2-L-P-5-6-P-8-9 (SEQ ID NO:10),
positioned anywhere along the peptide. In the above-mentioned
10 formula, each number represents an amino acid residue, such that 2 represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, 8 represents any amino acid residue except cysteine, and 9 represents a hydrophilic amino acid residue except cysteine. Each letter used
15 in the formulas herein represent the standard one-letter symbol for the corresponding amino acid. When the peptide is a 9-mer, the peptide R-P-L-P-P-L-P-T-S (SEQ ID NO:11) is excluded. The peptides of particular interest are those that exhibit a binding affinity for the SH3 domain of Src and Src-related proteins,
20 including Yes, Fyn, Lyn, Lck, Hck and Fgr. Preferably, the peptides of the invention exhibit a binding affinity for the SH3 domain of Src, which is at least three-fold, more preferably at least four-fold, most preferably at least about five-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9). In
25 still other embodiments, the peptides exhibit a binding affinity for the SH3 domain of Src which is at least ten-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9).

In specific embodiments, peptides are disclosed in which the various amino acid residues at the indicated positions may
30 independently have the following preferred identities: 2 is a P, R, A, L, Q, E or S, more preferably P or R; 5 represents a P, M, I or L, more preferably P or M; 6 is a P, L, I or V, more preferably P or L; 8 is a T, R, P, I, N, E, V, S, A, G or L, more preferably T or R; and 9 is a T, R, S, H or D, more preferably T
35 or R. Despite the preference for hydrophobic amino acid residues

at 5 and 6, in some cases it may be desirable to have hydrophilic amino acid residues at these positions. Specifically, amino acid residue 5 may be a T, R or S, and amino acid residue 6 may be a T or R. Likewise, while a hydrophilic amino acid residue is preferred at position 9, in some instances a hydrophobic residue, such as a P or A, may be desirable.

The present invention also contemplates SH3 domain-binding peptides with a minimum length of 10, 11, 12, 13, 14, 15 or more amino acids. Such peptides contain additional amino acid residues flanking the core sequence of R-2-L-P-5-6-P (SEQ ID NO:71) either at the C-terminal end, the N-terminal end or both. Thus, for example, such peptides include those that further comprise a C-terminal-flanking amino acid sequence of the formula 10, 10-11, 10-11-12, 10-11-12-13 (SEQ ID NO:12) or 10-11-12-13-14 (SEQ ID NO:13), in which each number represents any amino acid residue except cysteine, such that the amino acid residue 10 is bound to the amino acid residue 9 by a peptide bond. In that case, specific embodiments include an amino acid residue 10 which is T, R, L, S, D, P, A or N, preferably T or R, an amino acid residue 11 which is R, P, A, Q, S or T, preferably R or P, an amino acid residue 12 which is P, S, R or T, preferably P or S, an amino acid residue 13 which is P, S, R, F, H or T, preferably P or S, and an amino acid residue 14 which is S, R, G or T, preferably, S or R.

Furthermore, peptides are also provided which further comprise an N-terminal-flanking amino acid sequence of the formula 1', 2'-1', 3'-2'-1' or 4'-3'-2'-1' (SEQ ID NO:14) in which each number represents any amino acid residue except cysteine, such that 1' is bound to R by a peptide bond. In such a case, specific embodiments are provided in which the amino acid residue 1' is T, P, S, N, F, W, K, H, Q or G, preferably T or P, wherein the amino acid residue 2' is S, T, G, P, R, Q, L, A or H, preferably S or T, wherein the amino acid residue 3' is R, S, P, G, A, V, Y or L, preferably S or T, and wherein the amino acid residue 4' is R, S, V, T, G, L or F, preferably R or S.

In a particular embodiment, a peptide is disclosed having at least thirteen and up to forty-five amino acid residues, including an amino acid sequence of the formula, 3'-2'-1'-R-2-L-P-5-6-P-8-9-10 (SEQ ID NO:15), positioned anywhere
5 along the peptide, in which each number represents an amino acid residue, such that 3', 2', 1', 2, 8, and 10 each represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the
10 standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src. Preferred 13-mers include, but are not limited to, those having an amino acid residue 5 which is a P or M, an amino acid residue 1' which is T, P, S or N, an amino acid residue 2' which is S or
15 T, an amino acid residue 3' which is R or S, and an amino acid residue 10 which is T or R. In all the SH3 domain-binding peptides described herein, the prohibition against the use of the hydrophilic amino acid residue cysteine (C) does not extend beyond the 7-mer "core" sequence and the additional amino acid
20 residues flanking the core up to a total (core + flanking) of about 20 amino acids. That is, the occasional use of a cysteine is not absolutely prohibited. What should be kept in mind is that the potential for the formation of intramolecular disulfide bonds, to form a cyclic structure, be minimized as much as
25 possible. Applicants have found that cyclized structures appear to be disfavored, at least with potential binding peptides of less than about 15 amino acid residues in length. The concern for the formation of cyclized structures comprising the core sequence diminishes with increasing size of the peptide.
30 Presumably, a large enough structure, though cyclic, may allow the critical core sequence to adopt a more or less linear conformation.

In particular, specific peptides are disclosed which exhibit binding affinities to SH3 domains. These include the peptides,
35 RSTPRPLPMLPTTR (SEQ ID NO. 62), RSTPRPLPPLPTTR (SEQ ID NO. 67),

GILAPPVPPRNTR (SEQ ID NO. 63), VLKRPLPIPPVTR (SEQ ID NO. 64),
GPHRRLPPTPATR (SEQ ID NO. 65), and ANPSPATRPLPTR (SEQ ID NO. 66).

Phage clones are also disclosed, along with the amino acid
sequences that are responsible for SH3 domain binding. These
5 phage clones are identified in Figure 5.

In other embodiments of the present invention, SH3 domain-
binding peptides are contemplated which have a total of 11, 13,
14, 18, 20, 22, 23, 25, 30, 36, 38 or 45 amino acid residues.

The peptides of the present invention, having been disclosed
10 herein, may be prepared by any number of practicable methods,
including but not limited to solution-phase synthesis, solid-
phase synthesis, protein expression by a transformed host,
cleavage from a naturally-derived, synthetic or semi-synthetic
polypeptide, or a combination of these techniques.

15 The SH3 binding peptides exhibit a wide range of biological
activity which includes the enhancement (or inhibition, depending
on the particular peptide or the nature of the peptide's target
molecule, in this case a protein bearing an SH3 domain) of the
natural function or biological activity of the peptide's target
20 molecule. For example, the interaction of the binding peptide of
the present invention could result in the modulation of the
oncogenic activity of the target molecule bearing the SH3 domain.
If the target molecule has, in turn, a natural binding partner or
ligand, the peptides of the present invention may also exhibit
25 antagonistic or agonistic activity in relation to the biological
activity of the natural binding partner.

Thus, it is an object of the present invention to provide a
method of activating Src or Src-related protein tyrosine kinases
by administering an effective amount of the SH3 domain-binding
30 peptides generally described herein. The intensity of the immune
response can thus be stimulated, for example, by the increased
production of certain lymphokines, such as TNF-alpha and
interleukin-1. As is generally known to those of ordinary skill
in the art, a more intense immune response may be in order in

certain conditions, such as in combating a particularly tenacious infection, viral or otherwise, or a malignancy.

Furthermore, in a specific embodiment of the present invention, a conjugate compound is contemplated which comprises the peptide of the present invention and a second chemical moiety. The second chemical moiety can be selected from a wide variety of chemical compounds including the peptide itself. Typically, however, the second chemical moiety is selected to be other than the peptide of the present invention, including but not limited to an amino acid, a peptide other than an SH3 binding peptide of the present invention, a polypeptide or protein (i.e., the conjugate is a fusion protein), a nucleic acid, a nucleoside, a glycosidic residue (i.e., any sugar or carbohydrate), a label or image-enhancing agent (including metals, isotopes, radioisotopes, chromophores, fluorophores (such as FITC, TRITC, and the like), and enzyme substrates), a drug (including synthetic, semisynthetic, and naturally-occurring compounds), small molecules (e.g., biotin, hormones, factors) and the like.

The peptide of the present invention can be conjugated to the second chemical moiety either directly (e.g., through appropriate functional groups, such as an amine or carboxylic acid group to form, for example, an amine, imine, amide, ester, acyl or other carbon-carbon bond) or indirectly through the intermediacy of a linker group (e.g., an aliphatic or aromatic polyhydroxy, polyamine, polycarboxylic acid, polyolefin or appropriate combinations thereof). Moreover, the term "conjugate," as used herein, is also meant to encompass non-covalent interactions, including but not limited to ionic, affinity or other complexation interactions. Preferably, such other non-covalent interactions provide definable, most preferably, isolatable chemical conjugate species.

As described further herein, the peptides of the present invention have been shown to localize within certain cellular compartments which contain Src or Src-related prot ins.

Consequently, the above-described conjugate can be utilized as a

delivery system for introduction of a drug to cells, tissues or organs that include SH3 domain-containing proteins.

It should also be pointed out that the present invention seeks to provide a recombinant construct comprising a nucleic acid or its complement that includes codons or nucleotide sequences encoding a peptide having a region that binds to an SH3 domain, preferably the Src SH3 domain. The recombinant nucleic acid may be a DNA or RNA polynucleotide.

In a specific embodiment, the present invention contemplates a recombinant construct which is a transforming vector. Such vectors include those well known to those of ordinary skill in the art, which effect the transfer or expression of the nucleotide sequence after introduction to a host, such as recombinant plasmid, phage or yeast artificial chromosome. These vectors may be closed circular loops or they may be linearized. The vectors contemplated include those that exist extrachromosomally after host transformation or transfection, as well as those that integrate within or even displace portions of the host chromosome. The vectors may be introduced to the cell with the help of transfection aids or techniques well-known in the art. For example, these aids or techniques may take the form of electroporation, use of calcium chloride, calcium phosphate, DEAE dextran, liposomes or polar lipid reagents known as LIPOFECTIN or LIPOFECTAMINE. In addition, the present invention contemplates the direct introduction of the desired nucleic acid to the host cell, for instance, by injection.

Transformed host cells are also obtained by the methods of the present invention which are capable of reproducing the polynucleotide sequences of interest and/or expressing the corresponding peptide products. A variety of hosts are contemplated, including prokaryotic and eukaryotic hosts. In particular, bacterial, viral, yeast, animal, and plant cells are potentially transformable hosts. Thus, a method is disclosed to obtain a transformed host cell that can produce, preferably secrete, a peptide having a region that binds to an SH3 domain

comprising (a) providing an expression vector, preferably a secretory expression vector, comprising a nucleotide sequence encoding at least one copy of a peptide having a region that binds to an SH3 domain; and (b) introducing the vector to a competent host cell.

The peptides, thus produced, may then be introduced to cells, tissues, organs, or administered to the subject for the purpose of modulating the biochemical activity of the SH3 domain-containing proteins present therein. Accordingly, in specific embodiments of the present invention, compositions are provided which comprise an SH3 domain-binding peptide, including a core sequence and flanking sequences, and a suitable carrier.

The compositions contemplated by the present invention may also include other components, from those that facilitate the introduction or administration of the compositions to those that have their own innate activity, such as a prophylactic, a diagnostic or a therapeutic action. Such innate activity may be distinct from that of the peptides of the present invention or be complementary thereto. In any event, the compositions of the present invention include those that are suitable for administration into mammals, including humans. Preferably, the compositions (including necessarily the carrier) of the present invention are sterile, though others may need only be cosmetically, agriculturally or pharmaceutically acceptable. Still other compositions may be adapted for veterinary use.

The compositions, including the drug delivery systems described herein, are contemplated to be administered in a variety of ways, such as parenterally, orally, enterally, topically or by inhalation. The compositions may also be administered intranasally, ophthalmically or intravaginally. Furthermore, the compositions of the invention can take several forms, such as solids, gels, liquids, aerosols or patches.

In another embodiment of the present invention a method is provided of identifying a peptide having a region that binds to an SH3 domain comprising: (a) providing an immobilized target

protein comprising an SH3 domain; (b) incubating the immobilized target protein with an aliquot taken from a phage-displayed random peptide library, which library includes peptides having a random sequence of ≥ 8 amino acid residues; (c) washing unbound phage from the immobilized target protein; (d) recovering the phage bound to the immobilized target protein; and (e) determining the relevant nucleotide sequence of said binding phage nucleic acid and deducing the primary sequence corresponding to the SH3 domain-binding peptide. Preferably, the method further comprises amplifying the titer of the recovered phage and repeating the steps of incubation, washing and recovery to provide SH3 domain-binding peptide-enriched phage.

Any other mode by which the peptide library, random or otherwise, can be "displayed" can be utilized in the present invention, however. Moreover, the present applicants believe that longer random peptide sequences (e.g., >6 amino acid residues, preferably >10 , and most preferably, >12) provide not only much greater diversity but also a richer degree of secondary structure conducive to binding activity. If the random region of the peptide is less than or equal to an 8-mer, it should preferably not be cyclized.

5.2. Preparation of Random Peptide Libraries

The preparation and characterization of the preferred phage-displayed random peptide libraries have been described elsewhere. See, for example, Kay, B.K. et al. in Gene (1992) 128:59-65, for a description of the preparation of the phage-displayed random peptide library known as TSAR-9, more below. In particular, by cloning degenerate oligonucleotides of fixed length into bacteriophage vectors, recombinant libraries of random peptides can be generated which are expressed at the amino-terminus of the pIII protein on the surface of M13 viral particles. (There are 3-5 copies of the pIII-fusion on the surface of each particle.) Phage display offers several conveniences: first, the expressed peptides are on the surface

of the viral particles and accessible for interactions; second, the recombinant viral particles are stable (i.e., can be frozen, exposed to pH extremes); third, the viruses can be amplified; and fourth, each viral particle contains the DNA encoding the recombinant genome. Consequently, these libraries can be screened by isolating viral particles that bind to targets. The isolates can be grown up overnight, and the displayed peptide sequence responsible for binding can be deduced by DNA sequencing.

These libraries have approximately $>10^8$ different recombinants, and nucleotide sequencing of the inserts suggests that the expressed peptides are indeed random in amino acid sequence. These libraries are referred to herein as TSAR libraries, where TSAR stands for Totally Synthetic Affinity Reagents. The preparation of the TSAR libraries are described further below.

5.3. SH3 Binding Clones And Their Characteristics

Accordingly, peptides have been isolated from an unconstrained random peptide library which exhibit a binding affinity for SH3 domains. Furthermore, the binding affinities exhibited by the disclosed peptides differ in their selectivities with certain peptides showing comparable binding affinities for SH3 domains derived from different proteins, while others manifest greater affinities for specific SH3 domains.

The amino acid sequence of various peptides isolated by the present method are listed in Figure 5. As can be seen from this list, certain groups of SH3 domain binding peptides are isolated from three separate random peptide libraries, each based on a different type of random peptide insert, all displayed at the amino-terminus of the pIII protein on the surface of M13 viral particles. Ten clones were isolated from the R8C library, seven from the TSAR-12 library, and seven from the TSAR-9 library. The sequences are presented to highlight the particular amino acid residues believed to bind directly to the SH3 domain, as well as

to point out the remaining amino acid residues of the random insert and the viral flanking sequences and complementary site amino acid residues common to each group of clones. The frequency with which each particular clone is found in each library is also indicated in Figure 5. Thus, clones T12.SRC3.1 and T12.SRC3.2 are by far the most abundant clones found among the three libraries.

Interestingly, all the binding peptides are found to have the proline-rich amino acid residue motif, which is apparently responsible for binding, the motif being located predominantly at the C-terminal end of the insert, although each clone also contains an insert at the N-terminal end. The significance of this observation is not presently understood, although this finding may indicate the possible importance of the C-terminal viral flanking sequences in SH3 domain binding.

Indeed, a synthetic peptide bearing only the core consensus sequence RPLPPLP (SEQ ID NO:9) was less effective in binding to target SH3 domains than synthetic peptides that also included additional amino acid residues flanking the core sequences.

Thus, 13-mers and 14-mers having the sequences RSTPRPLPMLPTTR (SEQ ID NO:62), RSTPRPLPPLPTTR (SEQ ID NO:67), GILAPPVPPRNTTR (SEQ ID NO:63), GPHRRLPPTPATR (SEQ ID NO:65), and VLKRPLPIPPVTR (SEQ ID NO:64) have been prepared and shown to bind to SH3 domains, such as those of Src and Yes, much more avidly than the 7-mer, RPLPPLP (SEQ ID NO:9). The 13-mer ANPSPATRPLPTR (SEQ ID NO:66) has been shown to have binding affinities comparable to the core consensus sequence. In each case, the 13-mers comprise a 7-mer "core" sequence plus additional amino acid residues flanking same, some of which additional amino acid residues are contributed by the viral flanking sequences.

Thus, in one embodiment of the present invention, a 7-mer core includes a consensus motif of the formula RXLP ϕ ϕ P (SEQ ID NO:71), wherein R is arginine, L is leucine, P is proline, X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue. By "hydrophobic amino acid

residue," the applicants mean to include F, Y, W, V, A, I, L, P or M, each letter representing the standard one-letter designation for the corresponding amino acid residue.

Furthermore, a preferred 9-mer peptide comprising two additional amino acids on the C-terminal end of the core sequence is envisioned having a consensus motif of the formula RXLP $\phi\phi$ PX ψ . In this preferred 9-mer consensus motif, the symbol ψ represents a hydrophilic amino acid residue, except cysteine. By "hydrophilic amino acid residue," the applicants mean to include K, R, H, D, E, N, Q, T, S or C, and the other symbols are as defined above. For the purposes of the present invention, a glycine residue (G) may be considered either a hydrophobic or a hydrophilic amino acid residue. The one-letter symbols B and Z, which stand for N or D and Q or E, respectively, are considered hydrophilic amino acid residues.

Particular 13-mer peptides of the present invention include those listed, below. It is noted, however, that not all the following 13-mer peptides correlate strictly to or comply with the preferred 9-mer consensus motif, described above. Those peptides that do not comply (indicated in italics, with the non-complying amino acid residues underscored) can, thus, be described as "resembling" those that do comply (indicated in normal type) with the preferred 9-mer consensus motif:

PGFRELPLPPSR (SEQ ID NO:72), AQRPLPIPPETR (SEQ ID NO:73),
 VLKRPLPIPPVTR (SEQ ID NO:64), *PPNSPLPLPTH*L (SEQ ID NO:74),
*TGRG*PLPLPNDS (SEQ ID NO:75), YSTRPVPPITRPS (SEQ ID NO:76),
*SHKS*RLPLPTRP (SEQ ID NO:77), YRFRALPSPPSAS (SEQ ID NO:78),
 GPHRRPLPTPATR (SEQ ID NO:65), LAQRQLPPTPGRD (SEQ ID NO:79),
 ALQRRPLPTPPPA (SEQ ID NO:80), PATRPLPTRPSRT (SEQ ID NO:81),
 YSTRPLPSRPSRT (SEQ ID NO:82), XPGRI~~LL~~LPSEPR (SEQ ID NO:83),
 SGGI~~L~~APPVPPRN (SEQ ID NO:84), RSTRPLPILPRTT (SEQ ID NO:85),
 STPRPLPMLPTTR (SEQ ID NO:86), STNRPLPMIPTTR (SEQ ID NO:87),
 RSTRPLPSLPITT (SEQ ID NO:88), STSRPLPSLPITT (SEQ ID NO:89),
 RSTRSLPPLPPTT (SEQ ID NO:90), RSTRQLPIPPTTT (SEQ ID NO:91),
 STPRPLPLIPTTP (SEQ ID NO:92), RSTRPLPPTPLTT (SEQ ID NO:93), and

RSTRPQPPPPITT (SEQ ID NO:94). Accordingly, other peptides not specifically disclosed, which either comply with or "resemble" the preferred 9-mer consensus motif, can be readily envisioned by those of ordinary skill in the art and are considered to be equivalent to those that are specifically disclosed above. In particular, non-compliance at positions 1 (S, G, and I, in place of R, are tolerated), 3 (V, A, and Q, in place of L, are tolerated), 4 (L, in place of P, is tolerated), 5 (hydrophilic amino acid residues, S, R, and T, are tolerated in place of a hydrophobic amino acid residue), 6 (hydrophilic amino acid residues, R and T, are tolerated in place of a hydrophobic amino acid residue), 7 (T, and S, in place of P, are tolerated), and 9 (P and A are tolerated in place of a hydrophilic amino acid residue) have been observed.

5.3.1. Binding Specificities

It has been discovered that certain of the binding peptides disclosed have a greater relative binding affinity for one SH3 domain over another. Referring now to Figure 8, the relative binding affinities of the various peptides described above toward different SH3 domain targets are graphically presented. As one can see, the relative binding affinities of the respective peptides can differ by orders of magnitude. Thus, as shown in Figure 8, the peptide GPHRRLPPTPATR (SEQ ID NO:65), having the relevant sequence of the phage clone identified as T12.SRC3.3, is specific to Src family SH3 domains, including, but not limited to, Src, Yes, Lck, Hck, Fgr, Fyn, and Lyn. This SH3 binding peptide has little affinity for SH3 domains derived from PLC γ or Grb2. On the other hand, the peptide GILAPPVPPRNTR (SEQ ID NO:63), corresponding to the relevant sequence of the phage clone T12.SRC3.1, which is one of the most abundant binding clones found by the present method, binds generically to a broad range of SH3 domains, including Src, PLC γ , and Grb2.

On an intermediate level, the present invention has also uncovered a peptide, VLKRPLPIPPVTR (SEQ ID NO:64), corresponding

to the relevant sequence of the phage clone T12.SRC3.6, which is Src preferential; that is, this peptide exhibits strong binding affinities for members of the Src family, some binding affinities for Grb2 proteins, but little binding affinities for PLC γ domains. The peptide ANPSPATRPLPTR (SEQ ID NO:66), corresponding to the relevant sequence of the phage clone T12.SRC3.2, also exhibits Src family specificity similar to GPHRRLPPTPATR (SEQ ID NO:65). The peptides RSTPRPLMLPTTR (R8C.YES3.5; SEQ ID NO:62) and RSTPRPLPPLPTTR (representative consensus motif; SEQ ID NO:67) are highly specific for SH3 domain of Src, Yes, and other Src-related proteins.

5.4. Further Discussion of Binding Experiments

At the outset it is apparent that the binding affinity of certain peptides to the SH3 domain of Src and Src-related proteins is governed by more than just the presence of the preferred core consensus sequences, RLPPLP (SEQ ID NO:9) or RLPMLP (SEQ ID NO:95; i.e., RLP(P/M)LP, SEQ ID NO:96). Thus, while the synthetic peptides RSTPRPLMLPTTR (R8C.YES3.5; SEQ ID NO:62) and RSTPRPLPPLPTTR (consensus; SEQ ID NO:67) exhibit a strong specific binding affinity for Src SH3, the other synthetic peptides tested also exhibited an avid binding affinity to SH3 domains relative to the 7-mer, RLPPLP (SEQ ID NO:9). These other peptides, GILAPPVPPRNTR (SEQ ID NO:63), VLKRPLPIPPVTR (SEQ ID NO:64), GPHRRLPPTPATR (SEQ ID NO:65), and ANPSPATRPLPTR (SEQ ID NO:66), sport core sequences and flanking sequences that do not closely adhere to the preferred core consensus sequences. Thus, these results suggest that binding affinity to SH3 domains is governed to a large extent by the nature of the amino acid residues flanking the core 7-mer sequence.

The binding characteristics of Src SH3-selected peptides was determined using synthetic biotinylated peptides corresponding to the sequences displayed by Src SH3-selected phage. These biotinylated peptides were assayed for direct binding to immobilized Src SH3-GST. Each of the five library-derived

peptides tested were found to bind to Src SH3-GST and Yes SH3-GST over background (Figure 8). Furthermore, a strong correlation was observed between the similarity of a given peptide to the preferred core consensus sequence RPLP(P/M)LP and the peptide's affinity for Src SH3-GST. The core sequence of the clone T12.SRC3.1 (GILAPPVPPRNTR; SEQ ID NO:63) appears to provide more generic SH3 domain-binding characteristics.

Experiments comparing the relative binding of various phage clones to SH3 domains taken from a variety of proteins demonstrated the preference of these clones for Src and Src-related SH3 domains over SH3 domains taken from other proteins.

It was further found that while the 7-mer having the consensus sequence RPLPPLP (SEQ ID NO:9) bound to Src SH3-GST only weakly, peptides comprising the consensus sequence flanked by residues encoded by one of the Src SH3-selected clones (R8C.YES3.5), RSTP (SEQ ID NO:97) at the N-terminal end and TTR at the C-terminal end, bound significantly better than any of the peptides tested (Figure 7). Thus, as stated previously, sequences that flank the RPLP(P/M)LP (SEQ ID NO:96) core appear to be important contributors to SH3 binding. It is further surmised that a peptide having or resembling the sequence RSTPAPPVPPRTTR (SEQ ID NO:98) should exhibit strong but generic binding to a variety of SH3 domains.

Similarly, it is observed that most of the Src SH3-binding motifs are located near the carboxy-terminus of the random peptides, adjacent to sequences which are fixed in every clone (Figure 5). The exceptional clones tend to possess sequences that resemble motifs that include fixed flanking sequences. This clustering contrasts with previous results, in which binding motifs are distributed throughout the random peptide. Kay, B.K., et al., in Gene (1993) 128:59-65.

The binding of the library-derived Src SH3-binding peptides was compared to that of peptides corresponding to proline-rich regions of natural proteins. Peptides corresponding to SH3-binding regions in human PI-3' Kinase (KISPPTPKPRPPRPLPV; SEQ ID

NO:69) and human SOS1.20 (GTVEPVPPPVPPIRRRPESA; SEQ ID NO:68), as well as a proline-rich region of the cytoskeletal protein vinculin (LAPPKPPLPEGEV; SEQ ID NO:70), bound Src SH3 less well than the library-derived peptides (Figure 7).

5 As mentioned above, the relative specificity of binding was explored. Thus, the relative binding of Src SH3-selected peptides to equal amounts of GST fusions to SH3 domains from different proteins was determined (Figure 8). While all of the library-derived peptides bound the Src and Yes SH3 domains almost
10 equally well, none of the peptides (with the exception of peptide T12.SRC3.1, the most divergent peptide tested) bound the SH3 domains of Grb2, Crk, Abl or PLC γ 1 appreciably. Thus, the library-derived peptides, in contrast with a peptide derived from SOS1, exhibit SH3 binding that is relatively specific for Src-
15 family members.

Next, it was determined whether the binding to the Src SH3 domain was qualitatively like the interactions of the SH3 domain and natural proteins found in cell lysates. Thus, radiolabeled proteins were prepared from NIH 3T3 cell lysates and
20 chromatographed over Src SH3-GST immobilized on glutathione linked Sepharose. SDS-PAGE shows that a number of proteins can be affinity purified in this manner. The synthesized peptides bind quite well to the Src SH3 domain, as they can compete the binding of radiolabeled proteins from cell lysates to immobilized
25 Src-GST, with an IC $_{50}$ of 1-10 mM (Figure 9). In conclusion, the peptides can efficiently block the interaction of cellular proteins with Src SH3 in vitro.

Moreover, *Xenopus laevis* oocytes injected with mRNA encoding constitutively active Src undergo progesterone-induced maturation
30 at an accelerated rate relative to oocytes injected with water or c-Src mRNA. Unger, T.F. and Steele, R.E. in Mol. Cell. Biol. (1992) 12:5485-5498. To explore the ability of the library-derived Src SH3-binding peptides to exert a biochemical effect in vivo, the influence of the peptides on the maturation of *Xenopus laevis* oocytes was examined. Hence, stage VI oocytes were
35

injected with peptide, exposed to progesterone, and scored for germinal vesicle breakdown. Figure 10 shows that the rate of maturation was accelerated by approximately one hour when oocytes were injected with the SH3-binding peptide consisting of RPLPPLP (SEQ ID NO:9) flanked by residues from clone T12.SRC3.6 (VLKRPLPIPPVTR; SEQ ID NO:64), but not with water or a peptide corresponding to a proline-rich segment of vinculin (LAPPKPPLPEGEV; SEQ ID NO:70) as controls. The magnitude of this effect is roughly equivalent to that seen with injection of mRNA encoding constitutively active Src. See, e.g., Figure 3B in Unger, T.F. and Steele, R.E., *supra*. This result suggests that the library-derived Src SH3-binding peptide is effectively relieving an inhibitory effect of the Src SH3 domain upon Src PTK activity. This model is consistent with a number of studies which have demonstrated an inhibitory effect of the Src SH3 domain upon Src kinase and transforming activity. See, e.g., Okada, M., et al., *supra*; Murphy, S.M., et al., *supra*; and Superti-Furga, G., et al., *supra*.

5.5. Diagnostic And Therapeutic Agents Based On SH3 Binding Peptides and Additional Methods of Their Use

As already indicated above, the present invention also seeks to provide diagnostic, prophylactic, and therapeutic agents based on the SH3 binding peptides described herein.

In one embodiment, diagnostic agents are provided, preferably in the form of kits, comprising an SH3 domain-binding peptide and a detectable label conjugated to said peptide directly, indirectly or by complexation, said peptide comprising: (i) a core sequence motif of the formula RXLP $\phi\phi$ P (SEQ ID NO:71), wherein X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue, including F, Y, W, V, A, I, L, P, M or G, each letter representing the standard one-letter designation for the corresponding amino acid residue; and

(ii) two or more additional amino acid residues flanking said core sequence at its C-terminal end, N-terminal end or both.

The diagnostic agents of the present invention can be used to detect the presence of SH3 domains of a generic or specific type in cells, tissues or organs either *in vitro* or *in vivo*. For *in vivo* applications, the diagnostic agent is preferably mixed with a pharmaceutically acceptable carrier for administration, either enterally, parenterally or by some other route dictated by the needs of the particular application.

In a particular embodiment, for example, an assay based on a fusion product is contemplated which comprises a Src SH3 domain-binding peptide of the invention and a substrate for deregulated or "activated" Src. For instance, a muscle biopsy, taken from a subject suspected of being infected by the Rous sarcoma virus, can be treated with an effective amount of the fusion product. By subsequent analysis of the degree of conversion of the substrate, one can potentially detect infection by the Rous sarcoma virus in the subject, particularly mammals, especially chickens. The presence of the retrovirus, which causes the expression of deregulated or "activated" Src, may thus be indicated by unusually high levels of Src as revealed by large amounts of the converted substrate. See, for example, Paxton, W.G. et al., in Biochem. Biophys. Res. Commun. (1994) 200(1):260-267 (detection of phosphorylated tyrosine and serine residues of angiotensin II AT1 receptor, a substrate of Src family tyrosine kinases); another suitable substrate may be the protein p68 (Fumagalli, S. et al., in Nature (1994) 368(6474):871-874; Taylor, S.J. and Shalloway, D., in Ibid. at 867-871.

Alternatively, the enzyme can be isolated by selective binding to a form of the SH3 domain-binding peptides of the present invention (e.g., biotin-peptide conjugate). After isolation of the protein-peptide conjugate complex (e.g., on a column comprising streptavidin), the activity of the enzyme can then be assayed by conventional methods to determine its level of protein kinase activity which can be taken as an indication of

the presence of the deregulated or "activated" form of the enzyme. An assay for Src kinase has been described by Klinz and Maness, in Neuroprotocols (a companion to Neuroscience) (1992) 1(3):224-231.

5 Moreover, the diagnostic agents of the invention can also serve as imaging agents of cells, tissues or organs, especially those that contain proteins with an SH3 domain. For example, neural cells (e.g., neurons, other areas of the brain), osteoclasts, osteoblasts, platelets, immune cells, and other
10 dividing cells are known to express or contain proteins with SH3 domains. Thus, an image can be taken of portions of the body to serve as a baseline for subsequent images to detect physiologic or biochemical changes in the subject's body. For instance, changes in the condition of cellular levels of Src or a
15 transformation of the cellular Src to an "activated" form may be detected using the diagnostic or imaging agents of the present invention.

Accordingly, it has been demonstrated that an SH3-binding peptide tagged with a fluorescence emitter can provide an image
20 of the cytoskeleton. The images are presented in Figure 11. As can be seen from Figure 11, panels A, B, and C show the fluorescence image that is obtained on treating NIH 3T3 fibroblasts with SH3 domain-binding peptides modified to include a fluorescent tag. In sharp contrast, panel D shows only a dark
25 image that is produced when the cells are treated with a proline-rich segment of vinculin as a control.

In another embodiment, an SH3 domain-binding peptide-horseradish immunoperoxidase complex or related immunohistochemical agent could be used to detect and quantitate
30 specific receptor molecules in tissues, serum or body fluids. In particular, the present invention provides useful diagnostic reagents for use in immunoassays, Southern or Northern hybridization, and *in situ* assays. Accordingly, the diagnostic agents described herein may be suitable for use *in vitro* or *in*
35 *vivo*.

In addition, the diagnostic or imaging agent of the present invention is not limited by the nature of the detectable label. Hence, the diagnostic agent may contain one or more such labels including, but not limited to, radioisotope, fluorescent tags, paramagnetic substances, heavy metals, or other image-enhancing agents. Those of ordinary skill in the art would be familiar with the range of label and methods to incorporate or conjugate them into the SH3 domain-binding peptide to form diagnostic agents.

In yet a further embodiment, pharmaceutical compositions are provided comprising an SH3 domain-binding peptide and a pharmaceutically acceptable carrier. In a specific embodiment of the invention, the pharmaceutical composition is useful for the modulation of the activity of SH3 domain-containing proteins. By "modulation" is meant either inhibition or enhancement of the activity of the protein target. Accordingly, a pharmaceutical composition is disclosed comprising an SH3 domain-binding peptide and a pharmaceutically acceptable carrier, said peptide comprising: (i) a 9-mer sequence motif of the formula RXLP $\phi\phi$ PX ψ (SEQ ID NO:10), wherein X represents any amino acid except cysteine, ϕ represents a hydrophobic amino acid residue, and wherein ψ is a hydrophilic amino acid residue except cysteine, each letter representing the standard one-letter designation for the corresponding amino acid residue; and, optionally, (ii) additional amino acid residues flanking the 9-mer sequence at its C-terminal end, N-terminal end or both, up to a total of 45 amino acid residues, including said 9-mer sequence. Preferably, the peptide comprises at least one, more preferably at least two, and most preferably at least three additional amino acids flanking the 9-mer sequence.

As stated above, the therapeutic or diagnostic agents of the invention may also contain appropriate pharmaceutically acceptable carriers, diluents and adjuvants. Such pharmaceutical carriers can be sterile liquids, such as water and oils including those of petroleum, animal, vegetable or synthetic origin, such

as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, magnesium carbonate, magnesium stearate, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. These compositions can take the form of solutions, suspensions, tablets, pills, capsules, powders, sustained-release formulations and the like. Suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin.

Such compositions will contain an effective therapeutic amount of the active compound together with a suitable amount of carrier so as to provide the form for proper administration to the subject. While intravenous injection is a very effective form of administration, other modes can be employed, including but not limited to intramuscular, intraperitoneal, and subcutaneous injection, and oral, nasal, enteral, and parenteral administration.

The therapeutic agents and diagnostic agents of the instant invention are used for the treatment and/or diagnosis of animals, and more preferably, mammals including humans, as well as dogs, cats, horses, cows, pigs, guinea pigs, mice and rats. Accordingly, other methods contemplated in the present invention, include, but are not limited to, a method of modulating, i.e., inhibiting or enhancing, bone resorption in a mammal (see, e.g., Hall, T.J., in Biochem. Biophys. Res. Commun. (1994) 199(3):1237-44), a method of disrupting protein tyrosine kinase-mediated signal transduction pathways or a method of regulating the processing, trafficking or translation of RNA in a cell by introducing or administering an effective amount of an SH3

domain-binding peptide of the present invention (see, e.g., Taylor, S.J. and Shalloway, D., *supra*).

The diagnostic or therapeutic agents of the present invention can be modified by attachment to soluble macromolecules such as proteins, polysaccharides, or synthetic polymers. For example, the peptide could be coupled to styrene-maleic acid copolymers (see, e.g., Matsumura and Maeda, Cancer Res. (1986) 46:6387), methacrylamide copolymers (Kopecek and Duncan, J. Controlled Release (1987) 6:315), or polyethylene glycol (PEG) (e.g., Hershfield and Buckley, N. Engl. J. Med. (1987) 316:589; Ho et al., Drug Metab. Dispos. (1986) 14:349; Chua et al., Ann. Intern. Med. (1988) 109:114). The agents, if desired, are further targeted by attachment to an antibody, especially a monoclonal antibody. Such antibodies include but are not limited to chimeric, single chain, Fab fragments, and Fab expression libraries. In one embodiment the agent is coupled to the macromolecule via a degradable linkage so that it will be released *in vivo* in its active form.

In another embodiment, the therapeutic or diagnostic agent may be delivered in a vesicle, in particular a liposome. See, Langer, Science (1990) 249:1527-1533; Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York (1989) pp. 353-365; Lopez-Berestein, ibid., pp. 317-327.

In yet another embodiment, the therapeutic or *in vivo* diagnostic agent can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, CRC Crit. Ref. Biomed. Eng. (1987) 14:201; Buchwald et al., Surgery (1980) 88:507; Saudek et al., N. Engl. J. Med. (1989) 321:574). In another embodiment, polymeric materials may be used (see Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida, 1974; Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.) Wiley, New York 1984; Raner and Peppas, J. Macromol. Sci. Rev. Macromol. Chem. (1983) 23:61; see, also, Levy et al.,

5 Science (1985) 228:190; During et al., Ann. Neurol. (1989)
25:351; Howard et al., J. Neurosurg. (1989) 71:105). In a
preferred embodiment, a controlled release system may be placed
next to the therapeutic target, thus requiring only a fraction of
the systemic dose (see, e.g., Goodson, in Medical Applications of
10 Controlled Release, supra, (1984) 2:115-138). It will be
recognized by one of ordinary skill in the art that a particular
advantage of the invention is that a peptide will not be subject
to the problems of denaturation and aggregation associated with
15 proteins held in the warm, moist environment of a body in a
controlled release system.

Other controlled release systems are discussed in the review
by Langer, in Science (1990) 249:1527-1533.

6. EXAMPLES

6.1. Preparation of the TSAR-9 Library

6.1.1. Synthesis and Assembly of Oligonucleotides

Figure 1 shows the formula of the oligonucleotides and the assembly scheme used in construction of the TSAR-9 library. The oligonucleotides were synthesized with an applied Biosystems 380a synthesizer (Foster City, CA), and the full-length oligonucleotides were purified by HPLC.

Five micrograms of each of the pair of oligonucleotides were mixed together in buffer (10 mM Tris-HCl, pH 8.3, 15 mM KCl, 0.001% gelatin, 1.5 mM magnesium chloride), with 0.1 % Triton X-100, 2 mM dNTP's, and 20 units of Taq DNA polymerase. The assembly reaction mixtures were incubated at 72 °C for 30 seconds and then 30 °C for 30 seconds; this cycle was repeated 60 times. It should be noted that the assembly reaction is not PCR, since a denaturation step was not used. Fill-in reactions were carried out in a thermal cycling, device (Ericomp, LaJolla, CA) with the following protocol: 30 seconds at 72 °C, 30 seconds at 30 °C, repeated for 60 cycles. The lower temperature allows for annealing of the six base complementary region between the two sets of the oligonucleotide pairs. The reaction products were phenol/chloroform extracted and ethanol precipitated. Greater than 90% of the nucleotides were found to have been converted to double stranded synthetic oligonucleotides.

After resuspension in 300 µL of buffer containing 10 mM Tris-HCl, pH 7.5, 1 mM EDTA (TE buffer), the ends of the oligonucleotide fragments were cleaved with *Xba* I and *Xho* I (New England BioLabs, Beverly, MA) according to the supplier's recommendations. The fragments were purified by 4% agarose gel electrophoresis. The band of correct size was removed and electroeluted, concentrated by ethanol precipitation and resuspended in 100 µL TE buffer. Approximately 5% of the assembled oligonucleotides can be expected to have internal *Xho* I or *Xba* I sites; however, only the full-length molecules were used

in the ligation step of the assembly scheme. The concentration of the synthetic oligonucleotide fragments was estimated by comparing the intensity on an ethidium bromide stained gel run along with appropriate quantitated markers. All DNA
5 manipulations not described in detail were performed according to Maniatis, *supra*.

To demonstrate that the assembled enzyme digested oligonucleotides could be ligated, the synthesized DNA fragments were examined for their ability to self-ligate. The digested
10 fragments were incubated overnight at 18 °C in ligation buffer with T4 DNA ligase. When the ligation products were examined by agarose gel electrophoresis, a concatamer of bands was visible upon ethidium bromide staining. As many as five different unit length concatamer bands (i.e., dimer, trimer, tetramer, pentamer,
15 hexamer) were evident, suggesting that the synthesized DNA fragments were efficient substrates for ligation.

6.1.2. Construction of Vectors

The construction of the M13 derived phage vectors useful for expressing a TSAR library has been recently described
20 (Fowlkes, D. et al. BioTech. (1992) 13:422-427). To express the TSAR-9 library, an M13 derived vector, m663, was constructed as described in Fowlkes. The m663 vector contains the pIII gene having a *c-myc*-epitope, i.e., as a stuffer fragment, introduced at the mature N-terminal end, flanked by *Xho* I and *Xba* I
25 restriction sites (see also, Figure I of Fowlkes).

6.1.3. Expression of the TSAR-9 Library

The synthesized oligonucleotides were then ligated to *Xho* I and *Xba* I double-digested m663 RF DNA containing, the pIII gene (Fowlkes) by incubation with ligase overnight at 12 °C.
30 More particularly, 50 ng of vector DNA and 5 ng of the digested synthesized DNA and was mixed together in 50 µL ligation buffer (50 mM Tris, pH 8.0, 10 mM MgCl₂, 20 mM DTT, 0.1 mM ATP) with T4 DNA ligase. After overnight ligation at 12°C, the DNA was

concentrated by ethanol precipitation and washed with 70% ethanol. The ligated DNA was then introduced into *E. coli* (DH5 α F'; GIBCO BRL, Gaithersburg, MD) by electroporation.

5 A small aliquot of the electroporated cells was plated and the number of plaques counted to determine that 10⁸ recombinants were generated. The library of *E. coli* cells containing recombinant vectors was plated at a high density (~400,000 per 150 mM petri plate) for a single amplification of the recombinant phage. After 8 hr, the recombinant bacteriophage were recovered
10 by washing each plate for 18 hr with SMG buffer (100 mM NaCl, 10 mM Tris-HCl, pH 7.5, 10 mM MgCl₂, 0.05% gelatin) and after the addition of glycerol to 50% were frozen at -80 °C. The TSAR-9 library thus formed had a working titer of ~2 x 10¹¹ pfu/ml.

6.2. Preparation of TSAR-12 Library

15 Figure 2 shows the formula for the synthetic oligonucleotides and the assembly scheme used in the construction of the TSAR-12 library. As shown in Figure 2, the TSAR-12 library was prepared substantially the same as the TSAR-9 library described in Section 6.1 above with the following exceptions:
20 (1) each of the variant non-predicted oligonucleotide sequences, i.e., NNB, was 30 nucleotides in length, rather than 54 nucleotides; (2) the restriction sites included at the 5' termini of the variant, non-predicted sequences were Sal I and Spe I, rather than Xho I and Xba I; and (3) the invariant sequence at
25 the 3' termini to aid annealing of the two strands was GCGGTG and CGCCAC rather than CCAGGT and GGTCCA (5' to 3').

After synthesis including numerous rounds of annealing and chain extension in the presence of dNTP's and Taq DNA polymerase, and purification as described above in Section 6.1.1, the
30 synthetic double stranded, oligonucleotide fragments were digested with Sal I and Spe I restriction enzymes and ligated with T4 DNA ligase to the nucleotide sequence encoding the M13 pIII gene contained in the m663 vector to yield a library of TSAR-expression vectors as described in Sections 6.1.2 and 6.1.3.

The ligated DNA was then introduced into *E. coli* (DH5 α F'; GIBCO BRL, Gaithersburg, MD) by electroporation. The library of *E. coli* cells were plated at high density (~400,000 per 150 mm petri plate) for amplification of the recombinant phage. After about 8 hr, the recombinant bacteriophage were recovered by washing, for 18 hr with SMG buffer and after the addition of glycerol to 50% were frozen at -80 °C.

The TSAR-12 library thus formed had a working titer of $\sim 2 \times 10^{11}$ pfu/mL.

6.3. Characterization of the TSAR-9 and -12 Libraries

The inserted synthetic oligonucleotides for each of the TSAR libraries, described in Sections 6.1 and 6.2 above, had a potential coding complexity of 20^{36} ($\sim 10^{47}$) and 20^{20} , respectively, and since $\sim 10^{14}$ molecules were used in each transformation experiment, each member of these TSAR libraries should be unique. After plate amplification the library solution or stock has 10^4 copies of each member/mL.

It was observed that very few (<10%) of the inserted oligonucleotide sequences characterized so far in both of the libraries have exhibited deletions or insertions. This is likely a reflection of the accuracy assembling the oligonucleotides under the conditions used and the fact that certain types of mutations (i.e., frame-shifts) would not be tolerated as pIII an essential protein for phage propagation.

In order to determine whether any coding bias existed in the variant non-predicted peptides expressed by these libraries, perhaps due to biases imposed in vitro during synthesis of the oligonucleotides or in vivo during expression by the reproducing phage, inserts were sequenced as set forth below.

6.3.1. Characterization of TSAR-9 Library

Inserted synthetic oligonucleotide fragments of 23 randomly chosen isolates were examined from the TSAR-9 library. Individual plaques were used to inoculate 1 ml of 2XYT broth

containing *E. coli* (DH5 α F') cells and the cultures were allowed to grow overnight at 37°C with aeration. DNA was isolated from the culture supernatants according to Maniatis, *supra*. Twenty-three individual isolates were sequenced according to the method of Sanger (Proc. Natl. Acad. Sci. USA (1979) 74:5463-5467) using as a primer the oligonucleotide 5'-AGCGTAACGATCTCCCG (SEQ ID NO. 99), which is 89 nucleotides downstream of the pIII gene cloning site of the m663 vector used to express the TSARS.

Nucleotide sequences and their encoded amino acid sequences were analyzed with the MacVector computer program (IBI, New Haven, CT). The Microsoft EXCEL program was used to evaluate amino acid frequencies. Such analyses showed that the nucleotide codons coding for and hence most amino acids, occurred at the expected frequency in the TSAR-9 library of expressed proteins. The notable exceptions were glutamine and tryptophan, which were over- and under-represented, respectively.

It is of interest to note the paucity of TAG stop codons in the inserts, i.e., only 2 of ~200 isolates characterized contained a TAG stop codon. About half [1-(47/48)³⁶] of the phage inserts were expected to have at least one TAG codon in view of the assembly scheme used. However, most of the TAG-bearing phage appear to have been lost from the library, even though the bacterial host was *supE*. This may be a consequence of suppression being less than 100% effective.

The amino acids encoded by the inserted double stranded synthesized oligonucleotide sequences, excluding the fixed PG-encoding centers, were concatenated into a single sequence and the usage frequency determined for each amino acid using the Microsoft EXCEL program. These frequencies were compared to that expected from the assembly scheme of the oligonucleotides, and the divergence from expected values represented by the size of the bars above and below the baseline. Chi square analysis was used to determine the significance of the deviations. The majority of amino acids were found to occur at the expected frequency, with the notable exceptions that glutamine and

tryptophan were somewhat over- and under-represented, respectively. Thus, except for the invariant Pro-Gly, any position could have any amino acid; hence, the sequences are unpredicted or random.

6.3.2. Characterization of TSAR-12 Library

Approximately 10 randomly chosen inserted oligonucleotides from the TSAR-12 library were examined by DNA sequencing as described above in Section 6.3.1. The isolates were chosen at random from the TSAR-12 library and prepared for sequencing, as were the TSAR-9 isolates. Analysis showed that except for the invariant Gly any position could have any amino acid; hence, the sequences are unpredicted or random.

6.4. Preparation of R8C Library

Referring now to Figure 3, two oligonucleotides were synthesized on an Applied Biosystems Model 380a machine with the sequence 5' -
TGACGTCTCGAGTTGTNNKNNKNNKNNKNNKNNKNNKNNKTGTGGATCTAGAAGGATC-3'
(SEQ ID NO:31) and 5'-GATCCTTCTAGATCC-3' (SEQ ID NO:32), where N is an equimolar ratio of deoxynucleotides A, C, G, and T, and K is an equimolar ratio of G and T. Fifty pmol of each oligonucleotide was incubated at 42 °C for 5 min, then 37 °C for 15 min, in 50 µL of Sequenase™ buffer (U.S. Biochemicals, Cleveland, OH) with 0.1 µg/µL acetylated BSA, and 10 mM DTT. After annealing, 10 units of Sequenase™ (U.S. Biochemicals) and 0.2 mM of each dNTP were added and incubated at 37 °C for 15 min. The sample was then heated at 65 °C for 2 hr, digested with 100 units of both Xho I and Xba I (New England BioLabs, Beverly, MA), phenol extracted, ethanol precipitated, and resolved on a 15% non-denaturing polyacrylamide gel. The assembled, digested fragment was gel purified prior to ligation. The vector, m663 (Fowlkes, D. et al. Biotech. (1992) 13:422-427), was prepared by digestion with Xho I and Xba I, calf alkaline phosphatase (Boehringer Mannheim, Indianapolis, IN) treatment, phenol

extracted, and purified by agarose gel electrophoresis. To
ligate, 20 μ g vector was combined with 0.2 μ g insert in 3 mL with
T4 DNA ligase (Boehringer Mannheim), according to the
manufacturer. After removal of the protein and buffer by phenol
5 extraction and ethanol precipitation, the ligated DNA was
electroporated into XL1-Blue *E. coli* (Stratagene, San Diego, CA)
and plated for eight hours at 37 °C. To recover the recombinant
phage, the top agar was collected with a spatula, mixed with an
equal volume of 100 mM NaCl, 10 mM MgCl₂, and 50 mM Tris-HCl
10 (pH7.5), and disrupted by two passes through an 18-gauge syringe
needle. The bacterial cells were removed by centrifugation, and
phage particles were collected by polyethylene glycol
precipitation and stored at -70 °C in 25% glycerol. The library
had 10⁸ total recombinants and a working titer of 6 x 10¹³ pfu/mL.

15 Members of the library were checked for inserts by the
polymerase chain reaction (Saiki, et al. Science (1988) 239:487-
491). Individual plaques on a petri plate were touched with a
sterile toothpick and the tip was stirred into 2xYT with *E.*
coli bacteria and incubated overnight at 37 °C with aeration.
20 Five microliters of the phage supernatant were then transferred
to new tubes containing buffer (67 mM Tris-HCl, pH 8.8/10 mM β -
mercaptoethanol/16.6 mM ammonium sulfate/6.7 mM EDTA/50 μ g bovine
serum albumin per mL), 0.1 mM deoxynucleotide triphosphates, and
1.25 units of Taq DNA polymerase (Boehringer Mannheim,
25 Indianapolis, IN) with 100 pmoles of oligonucleotide primers.
The primers flanked the cloning site in gene III of m663 (5'-
TTCACCTCGAAAGCAAGCTG-3' (SEQ ID NO:100) and
5'-CCTCATAGTTAGCGTAACG-3' (SEQ ID NO:101)). The assembly
reactions were incubated at 94 °C for 1 min, 56 °C for 2 min, and
30 72 °C for 3 min; this cycle was repeated 24 times. The reaction
products were then resolved by electrophoresis on a NuSieve 2.0%
agarose gel (FMC, Rockland, ME). Gels revealed that for 20
plaques tested, all were recombinant and had single inserts of
the expected size.

Based on the sample size of the library, it was anticipated that 100% of the recombinants had single inserts. However, all of the SH3-binding phage isolated from the R8C library had double-inserts. Such phage are presumed rare (i.e., <5%) within the library, yet because the SH3-binding peptide appears to need to be linear they were selected for by our screening methods. Most likely they were formed during the generation of the library; one scenario is that the inserts ligated together to form head-to-head dimers and that they were subsequently cloned into m663 DNA by ligation with the vector's *Xho I* sticky end and by illegitimate ligation with the vector's *Xba I* site (see, Figure 4).

6.5. Preparation Of Target-Coated Microtiter Wells

6.5.1. Preparation Of GST-SH3 Fusion Proteins

The preparation of Src-GST fusion protein was first described by Smith and Johnson, in Gene (1988) 67:31, the disclosure of which is incorporated by reference herein. Briefly, pGEX-derived (Pharmacia, Piscataway, NJ) constructs expressing GST fusion proteins containing the SH3 domains of Src, Grb2, Crk, Abl, or PLC γ were obtained from Dr. Channing Der (University of North Carolina at Chapel Hill); a construct expressing the SH3 domain of Yes was obtained from Dr. Marius Sudol (Rockefeller University). The use of the pGEX bacterial expression vector for the production of GST-SH3 fusion proteins is well-known to those in the art. See, e.g., Cicchetti, P. et al., in Science (1992) 257:803-806. Briefly, the coding region for a particular SH3 domain can be fused in-frame at the Bam HI site of pGEX-2T. Thus, fusion proteins were prepared as per the manufacturer's instructions, and quantified by Coomassie Blue staining of SDS-polyacrylamide gels. Microtiter wells were coated with 5-20 μ g GST-SH3 fusion protein in 100 mM NaHCO $_3$, pH 8.5, blocked with 100 mM NaHCO $_3$ (pH 8.5) 1% BSA, and washed. All washes consisted of five applications of 1XPBS, 0.1% Tween 20, 0.1% BSA (Buffer A). Where appropriate, the amount of protein

bound to each well was quantified with an anti-GST antibody-based ELISA (Pharmacia, Piscataway, NJ), and with a GST-binding phage, isolated during the course of this work.

6.5.2. Coating of Microtiter Wells

5 Bacterially expressed Src SH3 glutathione-S-transferase (Src-GST) fusion protein was purified from bacterial lysates using glutathione agarose 4B (Pharmacia), according to the manufacturer's instructions. Bound Src-GST fusion protein was eluted from the glutathione agarose with 10 mM glutathione in
10 PBS. Microtiter wells were then coated with Src-GST fusion protein (1-10 μ g/well, in 50 mM NaHCO₃, pH 8.5) overnight at 4 °C. To block non-specific binding of phage, 100 μ L 1% BSA in 100 mM NaHCO₃, pH 8.5, was added to each well and allowed to incubate at room temperature for 1 hour. The wells were then washed five
15 times with 200 μ L PBS, 0.1% Tween 20, 0.1% BSA (Buffer A).

6.6. Biopanning And Subsequent Characterization Of Phage-Displayed Random Peptide Libraries With Src-GST Fusion Protein As Target Molecule

6.6.1. Isolation of Src SH3-Binding Phage

20 Library screens were performed as previously described. Kay, B.K., et al., in Gene (1993) 128:59-65. Briefly, 1 X 10¹¹ pfu TSAR 9, TSAR 12, or R8C phage in Buffer A were incubated in a Src SH3-GST-coated well for 2 hours. The wells were washed, and bound phage were eluted with 100 μ L 50 mM
25 glycine-HCl (pH 2.2), transferred to a new well, and neutralized with 100 mL 200 mM NaHPO₄ (pH 7.0). Recovered phage were used to infect 1 x 10⁹ DH5 α F' *E. coli* cells in 20 mL 2xYT; the infected cells were grown overnight, resulting in a 1000- to 10,000-fold amplification of phage titer. Amplified phage were panned twice
30 more, as above, excepting the amplification step. Binding phage recovered after the third round of panning were plated at a low density on a lawn of DH5 α F' *E. coli* cells to yield isolated plaques for clonal analysis. Isolated plaques were used to produce small cultures from which phage stocks and DNA were

recovered for phage binding experiments and dideoxy sequencing (Sanger, F., et al., in Proc. Natl. Acad. Sci. USA (1977) 74:5463-5467), respectively. Clones were confirmed as binding the SH3 domain by applying equal titers of phage to wells containing Src SH3-GST or GST alone, and titering the number of eluted particles from each well, or detecting bound phage with an anti-phage antibody-based ELISA (Pharmacia).

Indeed, the ability of isolated phage clones to bind to several SH3 domains derived from a variety of different proteins can be investigated by the manner described above. GST-SH3 fusion proteins containing SH3 domains from a variety of different proteins are bound to microliter wells. An aliquot of the aforementioned phage stocks (50 μ L) is introduced into wells containing the different GST-SH3 fusion proteins. After room temperature incubation for 1-2 hours, the liquid contents of the microtiter plates are removed, and the wells are washed 5 times with 200 μ L Buffer A. Bound phage are eluted with 100 μ L 50 mM glycine (pH 2.2), transferred to a new well, and neutralized with 100 μ L 200 mM NaHPO₄ (pH 7.0). The phage are diluted 10⁻³- to 10⁻⁶-fold, and aliquots are plated onto lawns of DH5 α F' *E. coli* cells to establish the number of plaque forming units in the output sample. From these experiments, the relative specificity of different Src SH3 binding clones for SH3 domains derived from other proteins is determined.

6.6.2. Phage ELISA and Nucleotide Sequencing

To evaluate the binding of isolates to various targets proteins, enzyme-linked-immuno-assays (ELISA) were also performed. Bacterial cultures were infected with phage isolates and cultured overnight in 2XYT at 37 °C. The cells were spun down and 25 mL of supernatant was added to microtiter plate wells coated with 50 mL of protein (1 mg/mL in 100 mM NaHCO₃, pH 8.4; overnight at 4 °C or for a few hours at room temperature) and blocked (1 mg/mL BSA in 100 mM NaHCO₃, pH 8.4; for about one hour). The phage are incubated in the well with 25 mL of

PBS-0.1% Tween 20 at RT for 2 hr. The wells are then washed multiple times over 30 minutes. To each well is added 50 μ L of polyclonal anti-phage antibody conjugated to horseradish peroxidase. The antibody is diluted 1:3000 in BSA-PBS-Tween 20; it was obtained from Pharmacia (Piscataway, NJ; catalog number 27-9402-01). After 30 minutes, the wells are washed again with BSA-PBS-Tween 20 for ~20 minutes. Finally, 100 μ L of ABTS reagent (Pharmacia, with H₂O₂) are added to each well for the development of color. Plates are read with a plate reader (Molecular Devices, Menlo Park, CA) at 405 nm wavelength.

The nucleotide sequence of the relevant segments of the Src SH3 binding clones (or phage clones that bind to SH3 domains of other proteins) were sequenced using standard methods. Sanger, F., et al., in Proc. Natl. Acad. Sci. USA (1977) 74:5463-5467. The oligo primer 5'-AGCGTAACGATCTAAA-3' (SEQ ID NO:102) was used, which is 89 nucleotides downstream of the gene III cloning site of M13 m666. The nucleotide sequences were analyzed with the MacVector computer program (IBI, New Haven, CT, USA). From this nucleotide sequence information the primary sequence of each Src SH3 binding peptide was deduced. The corresponding synthetic peptides were then prepared by techniques well known in the art with or without flanking sequences. Indeed, these synthetic peptides have been shown to bind to SH3 domain targets, with those possessing the phage flanking amino acid residues exhibiting greater binding affinity.

6.7 In Vitro Peptide Binding Assays

Peptides were obtained from Research Genetics (Birmingham, AL), Chiron Mimotopes (Victoria, Australia), or synthesized by conventional techniques by Dr. J. Mark Carter of Cytogen Corporation (Princeton, NJ). Peptide purity was assessed by HPLC and/or mass spectrometry. Biotinylated peptides were synthesized with either a KSGSG (SEQ ID NO:103) or a GSGS (SEQ ID NO:104) peptide linker (a spacer) between the biotin and the N-terminus of the peptide. Binding experiments were performed as

above, excepting the use of 10 μ M peptide instead of phage. Bound biotinylated peptide was detected with streptavidin conjugated to alkaline phosphatase (Sigma Chemical Co., St. Louis, MO). After one hour incubation period at room temperature, the wells were washed, and a solution of 3 mM p-nitrophenyl-phosphate (US Biochemicals, Cleveland, OH) in 50 mM NaCO₃ (pH 9.8), and 50 mM MgCl₂ was added and color allowed to develop. Signals were read with an ELISA plate reader (Molecular Devices, Menlo Park, CA) at 405 nm wavelength. Binding experiments were performed in triplicate. The results are presented in Figures 7 and 8.

6.8. Peptide Competition of GST-SH3 Affinity Precipitations of Cell Lysates

Labeled proteins are prepared by incubating a culture of HeLa cells overnight with ≥ 100 μ Ci/mL ³⁵S-methionine. The cells are then washed and lysed with mild detergent. This mixture of radioactive proteins is incubated with Src-GST fusion protein that has been immobilized on glutathione-linked Sepharose beads (Pharmacia, Piscataway, NJ). After several hours of tumbling, the beads are pelleted gently by low-speed centrifugation, and the supernatant is discarded. The beads are then resuspended into a slurry in PBS-0.1% Tween 20, pelleted, and washed several additional times. Finally, a 2% SDS solution is added to the sample, which is then boiled at 100 °C for 3 minutes. Afterward, the sample is centrifuged, and the supernatant loaded on a 10% polyacrylamide SDS gel for electrophoresis. After the proteins have been resolved, the gel is fixed, dried down, and exposed to X-ray film for autoradiography or phosphor plates for scanning by a Molecular Dynamics PhosphorImager.

The ability of Src SH3 to bind certain ³⁵S-labeled proteins is examined for competability with exogenous peptides. Synthetic peptides corresponding to phage-displayed inserts and motifs are added at the time that the lysate is incubated with the Src-GST

fusion protein immobilized on glutathione-linked sepharose beads. The SH3 binding peptides block binding of all or some of the labeled proteins while negative control peptides (unrelated peptide sequences) do not. The amount of competition is
5 quantified and correlated with the amount of added SH3-domain binding peptides.

Alternatively, NIH 3T3 cells were grown in Dulbecco's Modified Eagle Medium (DME) + 10% fetal calf serum (FCS) + 80 μ Ci/mL Tran³⁵Slabel (ICN), washed with PBS, lysed in RIPA buffer,
10 and pelleted. Supernatant from 1.5×10^6 cells was precleared with 100 μ g glutathione-agarose-immobilized GST. The supernatant was then incubated with 10 μ g glutathione-agarose-immobilized GST-SH3 fusion protein with or without added test peptide in a final volume of 250 μ L. Pelleted beads were washed with 1 mL
15 each of RIPA, RIPA + 1% deoxycholate + 0.1% SDS, and PBS, resuspended in 50 μ L SDS-PAGE sample buffer, boiled, and subjected to SDS-PAGE (7.5%). Labeled proteins were detected by phosphorimaging (Molecular Dynamics). The results are presented in Figure 9.

20 6.9. Peptide Competition of GST-SH3 Affinity Precipitations of PI-3' Kinase From Cell Lysates

It is possible to follow the precipitation of PI-3' Kinase by Src from cell lysates in the presence or absence of SH3-binding peptides. HeLa cells are lysed with detergent and
25 the protein mixtures are incubated for several hours with the Src-GST fusion protein immobilized on glutathione-linked Sepharose beads. After several hours of tumbling, the beads are pelleted gently by low-speed centrifugation and the supernatant is discarded. The beads are then resuspended into a slurry in
30 PBS-0.1% Tween 20, pelleted, and washed several additional times. Finally, an SDS solution is added to the sample, which is then boiled at 100 °C for 3 minutes. Subsequently, the sample is centrifuged, and the supernatant is loaded on a 10% polyacrylamide SDS gel for electrophoresis. After the proteins

have been resolved, the gel is blotted to nitrocellulose or nylon (i.e., western blot). The filter is then probed with a PI-3' Kinase antibody (monoclonal and polyclonal antibodies are available from Upstate Biotechnology Incorporated, Lake Placid, NY) and an enzyme-linked secondary antibody. The amount of PI-3' Kinase is then quantitated.

The ability of Src SH3 to bind PI-3' Kinase is examined for competability with exogenous peptides. Synthetic peptides corresponding to phage-displayed inserts and motifs are added at the time that the lysate is incubated with the Src-GST fusion protein that has been immobilized on glutathione-linked sepharose beads. Ten-fold and one hundred-fold molar excess of peptides are used relative to SH3 proteins. The SH3 binding peptides block binding of the PI-3' Kinase as detected on western blots while negative control peptides (unrelated peptide sequences) do not. The amount of competition is quantified and correlated with the amount of added SH3-domain binding peptides.

6.10. In Vivo Association Of SH3-Binding Peptides With SH3-Domains Of Proteins

To demonstrate association of the SH3-binding peptides with SH3-domains of proteins inside cells, the SH3-binding peptides are tagged and localized in cells. For example, Bar-Sagi et al., in Cell (1993) 74:83-91, have shown that SH3-binding proteins localize to the cytoskeleton when expressed in cells. Thus, the SH3 domain-binding peptides of the present invention can serve as cellular targetting signals (e.g., to the cytoskeleton). Accordingly, the peptides are tagged with biotin and, subsequently, injected into cells. Alternatively, one can transfect into cells a recombinant plasmid that expresses a fusion protein comprising of the SH3-binding peptide and the green fluorescent protein (GFP, Chalfie et al., in Science (1994) 263:802-805). The location of the biotinylated peptide or the GFP fusion protein is then assayed with FITC-labeled streptavidin in paraformaldehyde-fixed cells or by direct fluorescence in

living cells, respectively. Localization of the SH3-binding peptides to the cytoskeleton demonstrates that the SH3-binding peptides can bind SH3-domain proteins *in vivo*. In addition, focal adhesions, which are rich in Src, are also sites of potential subcellular localization of SH3-binding peptides.

Thus, NIH 3T3 fibroblasts were cultured *in vitro* on glass coverslips coated with fibronectin. After two days of growth at 37 °C, the cells were fixed for one hour at room temperature in the presence of 2% paraformaldehyde (pH 7.5). The coverslips were washed with PBS-0.1% Tween 20 several times to remove the fixative. Next, the coverslips were dipped into acetone (chilled at -20 °C) for approximately 20 seconds and allowed to air-dry. The coverslips were washed again with PBS-0.1% Tween 20, containing BSA (1 mg/mL), and incubated for 2 hours at room temperature with different biotinylated peptides in PBS-0.1% Tween 20. The coverslips were washed and then incubated with 1 mg/mL streptavidin-Cy3 (Jackson ImmunoResearch Co., West Grove, PA) for 1 hour at room temperature. Finally, the coverslips were washed in PBS-0.1% Tween 20, mounted in a glycerol solution on a glass slide, and viewed with a Nikon Optiphot epifluorescence microscope and a 60x oil immersion lens.

The results are presented in Figure 11, in which panel A displays cells stained with the conjugate biotin-spacer-VLKRPLPIPPVTR (SEQ ID NO:64); panel B exhibits cells stained with the conjugate, biotin-spacer-GILAPPVPPRNTR (SEQ ID NO:63); panel C shows cells stained with the long consensus peptide, biotin-spacer-RSTPRPLPPLPTTR (SEQ ID NO:67); and panel D shows cells stained with the proline-rich vinculin peptide conjugate, biotin-spacer-LAPPKPPLPEGEV (SEQ ID NO:70). The "spacer" sequence is KSGSG (SEQ ID NO:103). As shown in Figure 11, the panels in which SH3 domain-binding peptides were used present a bright display of fluorescence activity that is in sharp contrast to the relatively "dark" features of panel D (non-SH3 domain binding vinculin segment). These results demonstrate further the ability of the SH3 domain-binding peptides of the present invention to

localize to protein targets (e.g., Src and Src-related proteins) within cells and provide an image thereof.

6.11. In Vivo Modulation Of Src In Oocytes With SH3-Binding Peptides

5 When *Xenopus laevis* oocytes are injected with mRNA encoding deregulated Src, there are dramatic cytological and biochemical changes in the oocyte (Unger, T.F. and Steele, R.E., in Mol. Cell. Biol. (1992) 12:5485-5498). The applicants have obtained the plasmid for generating Src mRNA, which is available from Dr. Robert Steele (University of California at Irvine).
10 Synthetic SH3-binding peptides are injected into oocytes that have been previously injected with Src mRNA. The state of the cytoskeleton is inspected visually by observing the arrangement of cortical pigment granules under a dissecting microscope. The
15 state of phosphorylation of several proteins is examined by western blotting with an anti-phosphotyrosine monoclonal antibody (4G10; Upstate Biotechnology Incorporated), as described in Unger and Steele, above.

6.12. Progesterone-induced *X. laevis* Oocyte Maturation

20 Segments of adult ovary were removed surgically and incubated in 0.1% collagenase type D (Boehringer Mannheim, Indianapolis, IN) in Ca²⁺-free OR2 (82.5 mM NaCl, 2.5 mM KCl, 1.0 mM MgCl₂, 1.0 mM Na₂HPO₄, 5.0 mM HEPES, and 3.8 mM NaOH, pH 7.6).
25 Oocytes were then washed 3-5 times with OR2 containing 1.0 mM CaCl₂ and allowed to recover in OR2 overnight at 18 °C. Stage VI oocytes were injected with 40 nL of 100 mM peptide or water. After injection, the oocytes were placed in OR2 with 2 mg/mL progesterone (Sigma, St Louis, MO) and incubated at 20 °C.
30 Oocytes were scored at hourly time points for germinal vesicle breakdown (GVBD).

Figure 10 presents the results of this experiment. As shown by the graph, oocytes injected with the SH3 domain-binding

peptide VLKRPLPIPPVTR (SEQ ID NO:64) exhibit a faster rate of progesterone-induced germinal vesicle breakdown relative to oocytes that had been injected with water or with the proline-rich vinculin peptide, LAPPKPPLPEGEV (SEQ ID NO:70). These results parallel those obtained by Unger and Steele, *supra*, who observed a gross alteration in the cortex of oocytes that had been injected with RNA encoding a deregulated Src variant ("active" Src) versus those injected with RNA encoding the wild-type Src ("cellular" Src). Also, as shown in Figure 3B of the Unger and Steele article, oocytes injected with deregulated or active Src RNA matured at a faster rate than oocytes injected with water or wild-type Src RNA.

The present results obtained with Src SH3 domain-binding peptides suggest that these peptides modulate the biochemical activity of "cellular" Src; in particular, it is proposed that at least some of the Src SH3 domain-binding peptides of the present invention upregulate the biochemical activity of "cellular" Src, which may be downregulated or inhibited in its normal state. Hence, the administration of the SH3 domain-binding peptides of the present invention can constitute a novel method of modulating the activity of Src or Src-related proteins. Specifically, certain of these peptides are able to activate Src-family proteins.

6.13. In Vivo Antagonism Of Src In Src Transformed Cells With SH3-Binding Peptides

The coding regions for SH3-binding peptides are cloned into vectors that direct their expression in animal cells. A bipartite gene is constructed, encoding a protein with *c-myc* epitope and SH3-binding peptide, which is transcribed from a strong constitutive promoter (e.g., SV40, CMV, HSV TK, calmodulin). The vector is introduced into either normal or Src-transformed cells via transfection (e.g., electroporation, calcium phosphate, liposomes, DEAE dextran). Transfected cells express the bipartite gene transiently in culture. To create

stable transformed cell lines, the vector carries a selectable marker (e.g., neomycin resistance) or transfection is performed in the presence of excess plasmid carrying a selectable marker (e.g., neomycin resistance) and cells selected for the marker.

5 Transfected cells are stained by immunofluorescence to detect expression of the bipartite protein. The hybridoma 9E10 secretes a monoclonal antibody that is highly specific for the *c-myc* epitope (EQKLISEEDLN [SEQ ID NO:105]; see, Evan, G.A. et al., in Mol. Cell. Biol. (1985) 5:3610-3616). This antibody is used in

10 immunofluorescence experiments to demonstrate that the bipartite protein is expressed inside the cells, and in some cases, localized to subcellular structures enriched in SH3 domain bearing proteins.

There are several controls used in these experiments.

15 First, cells are transfected with vectors that do not have the SH3-binding peptide coding region. Second, normal (non-transformed) cells are transfected. Third, cells transformed by oncogenes other than *Src* are used in the transfection experiments. Fourth, cells are stained with other monoclonal

20 antibodies that do not recognize the *c-myc* epitope.

Transfected cells are examined for any changes in cell shape, behavior, and metabolism as a consequence of expressing the SH3 binding peptides. Cell shape is examined by phase contrast microscope at several times after transfection; in

25 particular, the flatness of the cells, their adhesion to the substrate, and the degree of cell ruffling are monitored. Cell division rates, cell migration, and contact inhibition are also observed over time. Finally, the amount of phosphorylated tyrosine in transfected cells is quantitated by phosphoaminoacid

30 analysis and with an anti-phosphotyrosine monoclonal antibody (4G10; Upstate Biotechnology Incorporated) in western blotting experiments.

6.14 Preparation of PXXP Biased Peptide Libraries

The preparation and characterization of preferred phage-displayed random peptide libraries have been described above in Sections 6.1 - 6.4.

5 Using procedures similar to those described in these sections, oligonucleotide inserts were constructed according to the schematic provided in FIG. 12. The inserts were then cloned into the mBAX vector, and the biased peptide libraries were expressed as described previously.

10 The mBAX vector was created in the Kay Laboratory by generating cloning sites in gene III of the M13mp18 vector (Messing, J. (1991). Cloning in M13 phage or how to use biology at its best. Gene 100, 3-12) in the manner of Fowlkes et al. (1992) (Biotechniques 13, 422-427). The mBAX vector displays a
15 peptide sequence at the N-terminus of the mature pIII protein that encodes the epitope for the mouse monoclonal antibody 7E11 (see, FIG. 13); it includes the stop codon TAG in the coding region, which is suppressed in *E. coli* carrying suppressor tRNA gene mutations known as *supE* or *supF*. There are no other stop
20 codons in the mBAX genome. The mBAX vector also carries a segment of the alpha fragment of β -galactosidase; bacterial cells expressing the omega fragment of β -galactosidase convert the clear XGal substrate into an insoluble blue precipitate. The
25 plaques appear blue.

30 Recombinant mBAX molecules can be distinguished easily from non-recombinant molecules due to the TAG codon in the *XhoI* - *XbaI* segment in gene III of mBAX. When recombinants are generated by replacing the *XhoI* - *XbaI* fragment with oligonucleotides encoding random peptides, the recombinants can be grown in
35 bacteria with (i.e., DH5 α F') or without (i.e., JS5) suppressor tRNA mutant genes. On the other hand, the non-recombinant mBAX molecules fail to produce plaques on bacterial lawns where the bacteria (i.e., JS5) lack such suppressor genes. This is because in JS5, the TAG codon serves as a stop codon to yield a truncated
pIII molecule during translation; since pIII is an essential

protein component of viable M13 viral particles, no plaques will form.

6.14.1 Discussion

The use of second generation or biased peptide libraries, which fix all or part of the RPLPPLP consensus motif for SH3 binding peptides and randomize flanking residues, has defined additional sequence residues exhibiting selective SH3 binding.

Tables 1-5, below, list the relevant amino acid sequences obtained from the biased peptide library for each set of SH3 domain binding peptides. The underscored amino acid residues indicate the fixed positions. Also, indicated for each set of new binders is a "consensus" sequence, which seeks to include the additional features gleaned from the new binding peptides. The symbol " ϕ " represents a hydrophobic residue.

TABLE 1 CORTACTIN SH3-BINDING PEPTIDES

		SEQ. ID NO.
PXXP.CORT.M1/2/3.PP	SSLLGPPVPPK <u>P</u> QTLFSFSR	107
PXXP.CORT.M4.PP	SRLGEFSK <u>P</u> PI <u>P</u> QKPTWMSR	108
PXXP.CORT.N2.PP	SRTERPPL <u>P</u> QRPDWLSYSSR	109
PXXP.CORT.N3.PP.INC	SREPDWLC <u>P</u> NC <u>P</u> LLLRSDSR	110
PXXP.CORT.01/2/3.PP	SSSSHNSR <u>P</u> PL <u>P</u> EKPSWLSR	111
PXXP.CORT.04.PP	SRLTPQSK <u>P</u> PL <u>P</u> PKPSAVSR	112
CONSENSUS	KPP ϕ P \times KP \times W R	113

TABLE 2

NCK SH3-BINDING PEPTIDES

		SEQ. ID NO.
PXXP.NCK.Q1/4.PP	<u>SSLGVGWKPLPPMRTASLSR</u>	114
PXXP.NCK.Q2/3.PP.INC	<u>SSVGFADRPRPPLRVESLSR</u>	115
PXXP.NCK.R1.PP.INC	<u>SSAGILRPPEKPxRSFSLSR</u>	116
PXXP.NCK.R2.PP	<u>SSPYTGDVPIPPLRGASLSR</u>	117
PXXP.NCK.R3.PP	<u>SSLMGSWPPVPPLRSDSLSR</u>	118
PXXP.NCK.R4.PP	<u>SSIGEDTPPSPPTRRASLSR</u>	119
PXXP.NCK.S1/4.PP	<u>SRSLSEVSPKPPIRSLSLSR</u>	120
PXXP.NCK.S2.PP.INC	<u>SSVSEGYSPLPPRSTLSR</u>	121
PXXP.NCK.S3.PP	<u>SSSFTLAAPTPTSLSLSR</u>	122
PXXP.NCK.T1.PP	<u>SSPPYELPPRPPNRTVLSLSR</u>	123
PXXP.NCK.T2.PP	<u>SRVVDGLAPPPVRLSSLR</u>	124
PXXP.NCK.T3.PP.INC	<u>SSLGYSGAPVPPHRxSSLR</u>	125
PXXP.NCK.T4.PP	<u>SSISDYSRPPPPVRTLSLSR</u>	126
CONSENSUS	ϕ xxxxxPxPP ϕ RSxSL T	127

TABLE 3

ABL SH3 BINDING PEPTIDES

		SEQ. ID NO.
PXXP.ABL.G1/2.PP	<u>SRGPRWSPPPVLPTSLDSR</u>	128
PXXP.ABL.G3/4.PP	<u>SSPPDYAAPAISSLWVDSR</u>	129
PXXP.ABL.H1/3/4.PP	<u>SSPPHWAPPAPPAMSPPI SR</u>	130
PXXP.ABL.H2.PP.INC	<u>SSDRWCWCPPWPAGGQRGSR</u>	131
PXXP.ABL.I1/2/3.PP	<u>SSPPKFSPPPPPYWLHASR</u>	132
PXXP.ABL.I4.PP	<u>SSPPSFAPPAAPRHSFGSR</u>	133
PXXP.ABL.J1.PP	<u>SSAPKKPAPPVPMMAHVMSR</u>	134
PXXP.ABL.J2.PP.INC	<u>SSPTYPPPPPPDTAKGASR</u>	135
PXXP.ABL.J3.PP.INC	<u>SSPPXXKPPPIPNSPQVLSR</u>	136
PXXP.ABL.J4.PP	<u>SSPPTWTPPKPPGWGVVFSR</u>	137
PXXP.ABL.L1.PP	<u>SSAPTWSPPALPNVAKYKSR</u>	138
PXXP.ABL.L2/3.PP	<u>SSIKGPRFPVPPVPLNGVSR</u>	139
PXXP.ABL.L4.PP	<u>SSPPAWSPPHRPVAFGSTSR</u>	140
CONSENSUS	PPxWxPPPφP	141

TABLE 4

PLCG SH3-BINDING PEPTIDES

		SEQ. ID NO.
PXXP.PLCG.P1.PP	<u>SSMKVHNFFLPPLPSYETSR</u>	142
PXXP.PLCG.P2.PP	<u>SRVPPLVAPRPPSTLNSLSR</u>	143
PXXP.PLCG.PE.PP.INC	<u>SSLYWQHGPDPVVGAPQLSR</u>	144
PXXP.PLCG.P4.PP	<u>SSHPLNSWPGGPFRHNLSSR</u>	145

TABLE 5 SRC SH3-BINDING PEPTIDES

		SEQ. ID NO.
PXXP.SRC.A1.PP	<u>SSRALVRPLPPVPGTSLSR</u>	146
PXXP.SRC.A2.PP	<u>SSFRALPLPPTPDNPFAGSR</u>	147
PXXP.SRC.A3.PP	<u>SRDAPGSLPFRPLPPVPTSR</u>	148
PXXP.SRC.A4.PP	<u>SSISQRALPPLPLMSDPASR</u>	149
PXXP.SRC.B1.PP	<u>SSPAYRPLRRLPDLSVIYSR</u>	150
PXXP.SRC.B2/3.PP	<u>SSFINRRLPALPPDNSLLSR</u>	151
PXXP.SRC.B4.PP	<u>SRLTGRPLPALPPPFSDFSR</u>	152
PXXP.SRC.C1.PP	<u>SRMKDRVLPPIPTVESAVSR</u>	153
PXXP.SRC.C2.PP.INC	<u>SSLYSAIAPDPPPRNSSSSR</u>	154
PXXP.SRC.C3.PP	<u>SSLASRPLPLLPNSAPGQSR</u>	155
PXXP.SRC.D1.PP	<u>SSLTSRPLPDIPVRPSKSSR</u>	156
PXXP.SRC.D2.PP.INC	<u>SSLKWRALPPLPETDTPYSR</u>	157
PXXP.SRC.D3.PP	<u>SSNTNRLPPPTPDGLDVRSR</u>	158
PXXP.SRC.D4.PP	<u>SSLQSRPLPLPPQSSYPISR</u>	159
CONSENSUS	RPLPPLP	160

It should be apparent to one of ordinary skill that many other embodiments of the present invention can be contemplated beyond the preferred embodiments described above but which other embodiments nevertheless fall within the scope and spirit of the present invention. Hence, the present invention should not be construed to be limited to the preferred embodiments described herein, which serve only to illustrate the present invention, but only by the claims that follow.

Also, numerous references are cited throughout the specification. The complete disclosures of these references are incorporated by reference herein.

SEQUENCE LISTING

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- (iii) NUMBER OF SEQUENCES: 106
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 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8
 - (D) OTHER INFORMATION: /note= "hydrophobic residue (such
as Pro or Leu)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Xaa Pro Xaa Xaa Pro Pro Xaa Xaa Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1..3
- (D) OTHER INFORMATION: /note= "Xaa = any residue other than Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "X = any residue other than Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8..9
- (D) OTHER INFORMATION: /note= "X = any residue other than Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Xaa Xaa Pro Pro Xaa Pro Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "X tends to be hydrophobic"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8..9
- (D) OTHER INFORMATION: /note= "X tends to be hydrophobic"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Xaa Leu Pro Pro Arg Pro Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
Arg Lys Leu Pro Pro Arg Pro Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
Val Pro Pro Pro Val Pro Pro Arg Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION: /note= "tends to be Pro"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /note= "hydrophobic residue"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "tends to be Pro"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
Xaa Xaa Xaa Pro Xaa Xaa Pro
1 5

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION: /note= "X = any residue other than Cys"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8..9
 - (D) OTHER INFORMATION: /note= "X = any residue other than Cys"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
Arg Xaa Leu Pro Pro Arg Pro Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /note= "hydrophobic residue"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
Arg Xaa Leu Pro Pro Leu Pro Arg Phe
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
Arg Pro Leu Pro Pro Leu Pro
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "any residue other than Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5..6
- (D) OTHER INFORMATION: /note= "any hydrophobic residue"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "any hydrophilic residue except Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Xaa Leu Pro Xaa Xaa Pro Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Pro Leu Pro Pro Leu Pro Thr Ser
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: C-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: C-terminal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: N-terminal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
Xaa Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1..3
 - (D) OTHER INFORMATION: /note= "any residue other than Cys"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "any residue other than Cys"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8..9
 - (D) OTHER INFORMATION: /note= "any hydrophobic residue"
- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 11..13
 - (D) OTHER INFORMATION: /note= "any residue other than Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Xaa Xaa Xaa Arg Xaa Leu Pro Xaa Xaa Pro Xaa Xaa Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Pro Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Arg
 35 40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGCTCGAGNN NBNNBNNBNN BNNBNNBNNB NNBNNBNNBN NBNNBNNBNN BNNBNNBNNB 60

NNBCCAGGT 69

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTCCANNVN NVNNVNNVNN VNNVNNVNNV NVNNVNNVNN NVNNVNNVNN VNNVNNVNNV 60

AGATCTGG 68

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCGAGNNNNBN NBNNBNNBNN BNNBNNBNNB NNBNNBNNBN NBNNBNNBNN BNNBNNBNNB	60
CCAGGT	66

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCCANNVN NVNNVNNVNN VNNVNNVNV NNVNNVNNVN NVNNVNNVNN VNNVNNVNV	60
AGATC	65

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "Arg or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5				10						15		
Xaa	Xaa	Xaa	Xaa	Pro	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				20				25						30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Arg	Pro	Ser	Arg	Thr			
				35				40					45			

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS: .
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Ser His Ser Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1          5          10          15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20          25          30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Arg Pro Ser Arg
35          40          45
Thr

```

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "Ser or Thr"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "Ser, Arg, Gly, Cys or Trp"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 15
 (D) OTHER INFORMATION: /note= "Val, Ala, Asp, Glu or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
1          5          10          15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg
20          25

```

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTTTGTCGAC NNNBNNBNNB NNBNNBNNBN NBNBNNBNN BNGCGGTG

48

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCCACNVNN VMNVNNVNV NNVNNVNVN NVNVNNVTG ATCATTTT

48

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGCCACNVNN VNVNVNVNV NNVNVNVNV NVNVNNVTG ATC

43

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCGACNNBN NBNBNNBNN BNNBNNBNN NBNBNNBNGCG GTG

43

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Ser or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /note= "Ser, Arg, Gly, Cys or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Val, Ala, Asp, Glu or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
1          5          10          15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Pro Ser Arg Thr
          20          25          30

```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Ser or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "Ser, Arg, Gly, Cys or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Val, Ala, Asp, Glu or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Ser His Ser Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1          5          10          15

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Pro Ser
          20          25          30

Arg Thr

```

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGACGTCTCG AGTTGTNNKN NKNNKNNKNN KNNKNNKNNK TGTGGATCTA GAAGGATC 58

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCTAGATCTT CCTAG 15

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TCGAGTTGTN NKNNKNNKNN KNNKNNKNNK NNKTGTGGAT 40

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAACANNMNN MNNMNNMNNM NNMNNMNNMA CACCTAGATC

40

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser	Ser	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Gly	Ser	Arg	Pro
1			5					10						15	

Ser Arg Thr

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser	Ser	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Gly	Ser	Arg	Ser
1			5					10					15	

Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Thr	Arg
			20					25			

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCGAGTTGTN NKNNKNNKNN KNNKNNKNNK NNKTGTGGAT CTAGATCCAC AVNNVNNVNN 60
 VNNVNNVNNV NNVNNACAAC 80

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Ser Phe Asp Gln Gln Asp Trp Asp Tyr Ser Ile Ala Glu Lys Met
 1 5 10 15
 His Pro Ile Arg Pro Gly Phe Arg Glu Leu Pro Pro Leu Pro Pro Ser
 20 25 30
 Arg Ala Ser Phe Gly Gly Gly Ala Ser Arg Pro Ser Arg
 35 40 45

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Thr Asn Val Trp Val Thr Gly Ser Val Ile Ala Arg Gly Ala Gln
 1 5 10 15
 Ser Arg Pro Leu Pro Ile Pro Pro Glu Thr Arg Pro Ser Arg
 20 25 30

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ser Thr Ala Pro Trp Gly Leu Arg Val Ala His Glu Gly Gly Val Leu
 1 5 10 15
 Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg Pro Ser Arg
 20 25 30

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

Ser Ser Ser Gly Tyr Val Val Pro Lys Arg Leu Gly Asp Met Arg Glu
1      5      10      15
Tyr Asn Ala His Pro Gly Leu His Val Pro Pro Asn Ser Pro Leu Pro
      20      25      30
Pro Leu Pro Thr His Leu Gln Ser Ser Arg Pro Ser Arg
      35      40      45

```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

Ser Ser Arg Gly Glu Gly Asn Asn Ile Ile Ser Ser Arg Pro Phe Leu
1      5      10      15
Ser Asn Ser Asp Pro Gly Val Ser Asn Lys Leu Thr Gly Arg Gly Pro
      20      25      30
Leu Pro Pro Leu Pro Asn Asp Ser Arg Pro Ser Arg
      35      40

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

Ser Thr Ala Val Ser Phe Arg Phe Met Pro Gly Gly Gly Gly Ala Phe
1      5      10      15
Tyr Ser Thr Arg Pro Val Pro Pro Ile Thr Arg Pro Ser Arg Thr
      20      25      30

```

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS: .
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Ser Thr Ala His Ser Leu Trp Asp Trp Gly Thr Phe Ser Gly Val Ser
1           5           10           15
His Lys Ser Arg Leu Pro Pro Leu Pro Thr Arg Pro Ser Arg Thr
                20           25           30

```

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

Pro Gly Tyr Ala Arg Ile Val Ser Tyr Arg Phe Arg Ala Leu Pro Ser
1           5           10           15
Pro Pro Ser Ala Ser Arg Pro Ser Arg
                20           25

```

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Ser Thr Asn Asp Val Asp Trp Met His Met Trp Asn Ser Gly Gly Pro
1           5           10           15
His Arg Arg Leu Pro Pro Thr Pro Ala Thr Arg Pro Ser Arg
                20           25           30

```

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

Ser Ser Asp Asn Trp Ala Arg Arg Val His Ala Ser Glu Leu Ile Tyr
1           5           10           15
Thr Asp Leu Ser Pro Gly Ile Leu Leu Ala Gln Arg Gln Leu Pro Pro
20           25           30
Thr Pro Gly Arg Asp Pro Ser His Ser Arg Pro Ser Arg
35           40           45

```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

Ser Ser Glu Ser Pro Leu Met Tyr Asn Arg Val Gly Ala Leu Gln Ser
1           5           10           15
Leu Thr Ser Val Pro Gly Ser Met Met His Phe Ala Leu Gln Arg Arg
20           25           30
Leu Pro Arg Thr Pro Pro Pro Ala Ser Arg Pro Ser Arg
35           40           45

```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

Ser Thr Arg Trp Ser His Ser Trp Pro Gly Tyr Val Gly Gly Ala Asn
1           5           10           15
Pro Ser Pro Ala Thr Arg Pro Leu Pro Thr Arg Pro Ser Arg Thr Val
20           25           30
Glu Ser Cys
35

```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Ser Arg Tyr Asn Asp Leu Gly Thr Arg Pro Val Ser Glu Val Ile Lys
1           5           10
Tyr Asp Tyr Phe Pro Gly Tyr Ser Gln His Val Ile Thr Pro Asp Gly
20           25           30
Ser Tyr Ser Thr Arg Pro Leu Pro Ser Arg Pro Ser Arg Thr Val Glu
35           40           45
Ser Cys
50

```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Pro Gly Arg Leu Leu Leu Pro Ser Glu Pro Arg Thr Phe Tyr Asn Tyr
1           5           10
Gly His Asp Ser Arg Pro Ser Arg
20

```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Ser Thr Met Tyr Gly Val Ser Trp Leu Ser Ser Gly Ser Gly Ile
1           5           10           15
Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg Pro Ser Arg
20           25           30

```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser	Ser	Cys	Thr	Glu	Lys	Thr	Val	Ser	Gly	Trp	Cys	Gly	Ser	Arg	Ser
1				5					10					15	
Thr	Arg	Pro	Leu	Pro	Ile	Leu	Pro	Arg	Thr	Thr	Arg	Pro	Ser	Arg	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ser	Ser	Cys	Met	Leu	Pro	Thr	Asp	Gly	Trp	Gln	Cys	Gly	Ser	Arg	Ser
1				5					10					15	
Thr	Pro	Arg	Pro	Leu	Pro	Met	Leu	Pro	Thr	Thr	Arg	Pro	Ser	Arg	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ser	Ser	Cys	Asp	Gly	Thr	Gln	Phe	Arg	Leu	Asn	Cys	Gly	Ser	Arg	Ser
1				5					10					15	
Thr	Asn	Arg	Pro	Leu	Pro	Met	Ile	Pro	Thr	Thr	Arg	Pro	Ser	Arg	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser	Ser	Cys	Met	Gln	Gly	Gln	Ala	Gly	Leu	Lys	Cys	Gly	Ser	Arg	Ser
1				5					10					15	
Thr	Arg	Pro	Leu	Pro	Ser	Leu	Pro	Ile	Thr	Thr	Arg	Pro	Ser	Arg	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ser	Ser	Cys	Tyr	Arg	Glu	Lys	Asp	Thr	Trp	Gly	Cys	Gly	Ser	Arg	Ser
1				5					10					15	
Thr	Ser	Arg	Pro	Leu	Pro	Ser	Leu	Pro	Thr	Thr	Arg	Pro	Ser	Arg	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ser	Ser	Cys	Leu	Phe	Glu	Gln	Gly	Ala	Gly	Thr	Cys	Gly	Ser	Arg	Ser
1				5					10					15	
Thr	Arg	Ser	Leu	Pro	Pro	Leu	Pro	Pro	Thr	Thr	Arg	Pro	Ser	Ser	Arg
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser	Ser	Cys	Asp	Thr	Gly	Arg	Ile	Ala	Pro	Gly	Cys	Gly	Ser	Arg	Ser
1				5					10					15	
Thr	Pro	Arg	Pro	Leu	Pro	Leu	Ile	Pro	Thr	Thr	Pro	Arg	Ser	Thr	Asn
			20					25					30		
Leu	Asn	Leu	Thr	Ser	Thr	Thr	Thr	Arg	Pro	Ser	Arg				
		35					40								

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ser	Ser	Cys	Gly	Leu	Asp	Asn	Ala	Ala	Lys	Thr	Cys	Gly	Ser	Arg	Ser
1				5					10					15	
Thr	Arg	Pro	Leu	Pro	Pro	Thr	Pro	Leu	Thr	Thr	Arg	Pro	Ser	Arg	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser	Ser	Cys	Ser	Arg	Ala	His	Glu	Thr	Glu	Met	Cys	Gly	Ser	Arg	Ser
1				5					10					15	
Thr	Arg	Pro	Gln	Pro	Pro	Pro	Pro	Ile	Thr	Thr	Arg	Pro	Ser	Arg	
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg	Ser	Thr	Pro	Arg	Pro	Leu	Pro	Met	Leu	Pro	Thr	Thr	Arg
1				5				10					

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Val Leu Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gly Pro His Arg Arg Leu Pro Pro Thr Pro Ala Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ala Asn Pro Ser Pro Ala Thr Arg Pro Leu Pro Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Arg Ser Thr Pro Arg Pro Leu Pro Pro Leu Pro Thr Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Gly Thr Val Glu Pro Val Pro Pro Pro Val Pro Pro Arg Arg Arg Pro
1 5 10 15

Glu Ser Ala

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro
1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Ala Pro Pro Lys Pro Pro Leu Pro Glu Gly Glu Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "any residue other than Cys"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5..6
 (D) OTHER INFORMATION: /note= "any hydrophobic residue"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Arg Xaa Leu Pro Xaa Xaa Pro
1 5

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Pro Gly Phe Arg Glu Leu Pro Pro Leu Pro Pro Ser Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala Gln Ser Arg Pro Leu Pro Ile Pro Pro Glu Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Pro Pro Asn Ser Pro Leu Pro Pro Leu Pro Thr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Thr Gly Arg Gly Pro Leu Pro Pro Leu Pro Asn Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Ser Thr Arg Pro Val Pro Pro Ile Thr Arg Pro Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser His Lys Ser Arg Leu Pro Pro Leu Pro Thr Arg Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Tyr Arg Phe Arg Ala Leu Pro Ser Pro Pro Ser Ala Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Leu Ala Gln Arg Gln Leu Pro Pro Thr Pro Gly Arg Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Leu Gln Arg Arg Leu Pro Arg Thr Pro Pro Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Pro Ala Thr Arg Pro Leu Pro Thr Arg Pro Ser Arg Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Tyr Ser Thr Arg Pro Leu Pro Ser Arg Pro Ser Arg Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS: .
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Xaa Pro Gly Arg Ile Leu Leu Leu Pro Ser Glu Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ser Gly Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Arg Ser Thr Arg Pro Leu Pro Ile Leu Pro Arg Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ser Thr Pro Arg Pro Leu Pro Met Leu Pro Thr Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ser Thr Asn Arg Pro Leu Pro Met Ile Pro Thr Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Arg Ser Thr Arg Pro Leu Pro Ser Leu Pro Ile Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Ser Thr Ser Arg Pro Leu Pro Ser Leu Pro Thr Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Arg Ser Thr Arg Pro Leu Pro Ser Leu Pro Ile Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Arg Ser Thr Arg Gln Leu Pro Ile Pro Pro Thr Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ser Thr Pro Arg Pro Leu Pro Leu Ile Pro Thr Thr Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Arg Ser Thr Arg Pro Leu Pro Pro Thr Pro Leu Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Arg Ser Thr Arg Pro Gln Pro Pro Pro Pro Ile Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Arg Pro Leu Pro Met Leu Pro
1 5

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "Pro or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Arg Pro Leu Pro Xaa Leu Pro
1 5

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Arg Ser Thr Pro
1

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Arg Ser Thr Pro Ala Pro Pro Val Pro Arg Thr Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AGCGTAACGA TCTCCCG

17

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TTCACCTCGA AAGCAAGCTG

20

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CCTCATAGTT AGCGTAACG

19

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AGCGTAACGA TCTAAA

16

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Lys Ser Gly Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Gly Ser Gly Ser
1

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Ser	Ser	Cys	Asp	His	Thr	Leu	Gly	Leu	Gly	Trp	Cys	Gly	Ser	Arg	Ser
1				5				10					15		
Thr	Arg	Gln	Leu	Pro	Ile	Pro	Pro	Thr	Thr	Thr	Arg	Pro	Ser	Arg	
		20						25					30		

WHAT IS CLAIMED IS:

1. A peptide having at least nine and up to forty-five amino acid residues, including an amino acid sequence of the formula, R-2-L-P-5-6-P-8-9 (SEQ ID NO:10), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 2 represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, 8 represents any amino acid residue except cysteine, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src, provided that said peptide is not R-P-L-P-P-L-P-T-S (SEQ ID NO:11).
2. The peptide of claim 1 in which 2 is a P, R, A, L, Q, E or S.
3. The peptide of claim 1 in which 5 is a P, M, I or L.
4. The peptide of claim 1 in which 6 is a P, L, I or V.
5. The peptide of claim 1 in which 8 is a T, R, P, I, N, E, V, S, A, G or L.
6. The peptide of claim 1 in which 9 is a T, R, S, H or D.
7. The peptide of claim 1 which further comprises a C-terminal-flanking amino acid sequence of the formula 10, 10-11, 10-11-12, 10-11-12-13 (SEQ ID NO:12) or 10-11-12-13-14 (SEQ ID NO:13), in which each number represents any amino acid residue except cysteine, such that 10 is bound to 9 by a peptide bond.
8. The peptide of claim 7 in which 10 is T, R, L, S, D, P, A or N.
9. The peptide of claim 7 in which 11 is R, P, A, Q, S or T.
10. The peptide of claim 7 in which 12 is P, S, R or T.
11. The peptide of claim 7 in which 13 is P, S, R, F, H or T.
12. The peptide of claim 7 in which 14 is S, R, G or T.
13. The peptide of claim 1 which further comprises an N-terminal-flanking amino acid sequence of the formula 1', 2'-1',

3'-2'-1' or 4'-3'-2'-1' (SEQ ID NO:14) in which each number represents any amino acid residue except cysteine, such that 1' is bound to R by a peptide bond.

14. The peptide of claim 13 in which 1' is T, P, S, N, F, W, K, H, Q or G.

15. The peptide of claim 13 in which 2' is S, T, G, P, R, Q, L, A or H.

16. The peptide of claim 13 in which 3' is R, S, P, G, A, V, Y or L.

17. The peptide of claim 13 in which 4' is R, S, V, T, G, L or F.

18. A peptide having at least thirteen and up to forty-five amino acid residues, including an amino acid sequence of the formula, 3'-2'-1'-R-2-L-P-5-6-P-8-9-10 (SEQ ID NO:15), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 3', 2', 1', 2, 8, and 10 each represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src.

19. The peptide of claim 18 in which 5 is a P or M.

20. The peptide of claim 18 in which 1' is T, P, S or N.

21. The peptide of claim 18 in which 2' is S or T.

22. The peptide of claim 18 in which 3' is R or S.

23. The peptide of claim 18 in which 10 is T or R.

24. The peptide of claim 1 the binding affinity of which is at least three-fold greater than that exhibited by the peptide RPLPPLP for the SH3 domain of Src.

25. The peptide of claim 18 the binding affinity of which is at least three-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9) for the SH3 domain of Src.

26. The peptide of claim 1 the binding affinity of which is at least four-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9) for the SH3 domain of Src.

27. The peptide of claim 18 the binding affinity of which is at least four-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9) for the SH3 domain of Src.

28. The peptide of claim 1 which further exhibits a general binding affinity for the SH3 domain of Abl, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, p85 PI-3'Kinase, and proteins related thereto.

29. The peptide of claim 1 which exhibits a selective binding affinity for the SH3 domain of Src and Src-related proteins.

30. The peptide of claim 18 which further exhibits a general binding affinity for the SH3 domain of Abl, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, p85 PI-3'Kinase, and proteins related thereto.

31. The peptide of claim 18 which exhibits a selective binding affinity for the SH3 domain of Src and Src-related proteins.

32. A peptide having the amino acid sequence RSTPRPLPMLPTTR (SEQ ID NO:62).

33. A peptide having the amino acid sequence RSTPRPLPPLPTTR (SEQ ID NO:67).

34. A peptide having the amino acid sequence GILAPPVPPRNTR (SEQ ID NO:63).

35. A peptide having the amino acid sequence VLKRPLPIPPVTR (SEQ ID NO:64).

36. A peptide having the amino acid sequence GPHRRLPPTPATR (SEQ ID NO:65).

37. A peptide having the amino acid sequence ANSPATRPLPTR (SEQ ID NO:66).

38. A peptide having an amino acid sequence selected from the group consisting of RSTRPLPILPRTT, STPRPLPMLPTTR, STNRPLPMIPTTR, RSTRPLPSLPITT, STSRPLPSLPPTTR, RSTRSLPPLPPTT,

RSTRQLPIPPTTT, STPRPLPLIPTTP, RSTRPLPPTPLTT, and RSTRPQPPPPITT
(SEQ ID NOS:85-94).

39. A peptide having the amino acid sequence selected from the group consisting of VLKRPLPIPPVTR (SEQ ID NO:64), YSTRPVPPITRPS (SEQ ID NO:76), SHKSRLPPLPTRP (SEQ ID NO:77), GPHRRLPPTPATR (SEQ ID NO:65), PATRPLPTRPSRT (SEQ ID NO:81), and SGGILAPPVPPRN (SEQ ID NO:84).

40. A peptide having the amino acid sequence selected from the group consisting of PPNSPLPPLPTH (SEQ ID NO:72), TGRGPLPPLPNDS (SEQ ID NO:74), YRFRALPSPPSAS, LAQRQLPPTPGRD ALQRRLPRTPPPA (SEQ ID NOS:78-80), YSTRPLPSRPSRT, and XPGRILLLPSEPR (SEQ ID NOS:82-83).

41. A construct comprising a nucleic acid encoding a peptide of claim 1 or its complement.

42. The construct of claim 41 which is a DNA polynucleotide.

43. The construct of claim 41 which is a RNA polynucleotide.

44. A construct comprising a nucleic acid encoding a peptide of claim 18 or its complement.

45. The construct of claim 44 which is a DNA polynucleotide.

46. The construct of claim 44 which is a RNA polynucleotide.

47. The construct of claim 41 which is a transforming vector.

48. The construct of claim 44 which is a transforming vector.

49. A host cell transformed with the vector of claim 47.

50. A host cell transformed with the vector of claim 48.

51. A conjugate comprising a peptide of claim 1 and a second molecule.

52. The conjugate of claim 51 in which said second molecule is selected from the group consisting of an amino acid, a

peptide, a protein, a nucleic acid, a nucleoside, a glycosidic residue, a label, a drug or a small molecule.

53. A diagnostic kit for the detection of SH3 domains comprising an SH3 domain-binding peptide and a detectable label conjugated to said peptide directly, indirectly or by complexation, said peptide comprising: (i) a core sequence motif of the formula RXLP $\phi\phi$ P (SEQ ID NO:71), wherein X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue, each letter representing the standard one-letter designation for the corresponding amino acid residue; and (ii) two or more additional amino acid residues flanking said core sequence at its C-terminal end, N-terminal end or both.

54. A drug delivery system comprising an SH3 domain-binding peptide and a drug conjugated to said peptide directly, indirectly or by complexation, said peptide comprising: (i) a core sequence motif of the formula RXLP $\phi\phi$ P (SEQ ID NO:71), wherein X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue, each letter representing the standard one-letter designation for the corresponding amino acid residue; and (ii) two or more additional amino acid residues flanking said core sequence at its C-terminal end, N-terminal end or both.

55. The drug delivery system of claim 54 which may be administered parenterally, orally, enterally, topically or by inhalation.

56. The drug delivery system of claim 54 which may be administered intranasally, ophthalmically or intravaginally.

57. The drug delivery system of claim 54 which is in the form of a solid, gel, liquid or aerosol.

58. A method of modulating the activity of Src or Src-related proteins comprising administering a composition comprising an effective amount of a peptide of claim 1 and a carrier.

59. The method of claim 58 which inhibits the activity of Src or Src-related proteins.

60. The method of claim 58 which activates Src or Src-related proteins.

61. A method of identifying a peptide having a region that binds to an SH3 domain comprising:

(a) providing an immobilized target protein comprising an SH3 domain;

5 (b) incubating said immobilized target protein with an aliquot taken from a random peptide library;

(c) washing unbound peptide from said immobilized target protein;

10 (d) recovering the peptide bound to said immobilized target protein; and

(e) determining the primary sequence of the SH3 domain-binding peptide.

62. The method of claim 61 in which said library is a displayed random peptide library.

63. The method of claim 62 in which said library is a phage-displayed random peptide library.

64. The method of claim 62 in which said library is a phagemid-displayed random peptide library.

65. The method of claim 61 in which step (c) includes washing unbound phage from said immobilized target protein; step (d) includes recovering the phage bound to said immobilized target protein; and step (e) includes determining the relevant
5 nucleotide sequence of said binding phage nucleic acid, from which the primary sequence corresponding to the SH3 domain-binding peptide is deduced.

66. A method of identifying a peptide having a region that binds to an SH3 domain comprising:

(a) providing an immobilized target protein comprising an SH3 domain;

5 (b) incubating said immobilized target protein with an aliquot taken from a phage-displayed random peptide library, which library includes peptides having a random sequence of ≥ 8 amino acid residues;

10 (c) washing unbound phage from said immobilized target protein;

(d) recovering the phage bound to said immobilized target protein; and

15 (e) determining the relevant nucleotide sequence of said binding phage nucleic acid and deducing the primary sequence corresponding to the SH3 domain-binding peptide.

67. The method of claim 66 which further comprises amplifying the titer of the recovered phage.

68. The method of claim 66 which further comprises repeating the steps of incubation, washing and recovery to provide SH3 domain-binding peptide-enriched phage.

69. A pharmaceutical composition comprising an SH3 domain-binding peptide and a pharmaceutically acceptable carrier, said peptide comprising: (i) a 9-mer sequence motif of the formula RXLP $\phi\phi$ PX ψ (SEQ ID NO:10), wherein X represents any amino acid
5 except cysteine, ϕ represents a hydrophobic amino acid residue, and wherein ψ is a hydrophilic amino acid residue except cysteine, each letter representing the standard one-letter designation for the corresponding amino acid residue; and, optionally, (ii) additional amino acid residues flanking said 9-mer sequence at its C-terminal end, N-terminal end or both, up to
10 a total of 45 amino acid residues, including said 9-mer sequence.

70. The composition of claim 69 in which at least one additional amino acid flanks said 9-mer sequence.

71. The composition of claim 69 in which at least two additional amino acids flank said 9-mer sequence.

72. The composition of claim 69 in which at least three additional amino acids flank said 9-mer sequence.

73. A method of disrupting protein tyrosine kinase-mediated signal transduction pathways comprising administering an effective amount of a peptide of claim 1.

74. A method of regulating the processing, trafficking or translation of RNA by administering an effective amount of a peptide of claim 1.

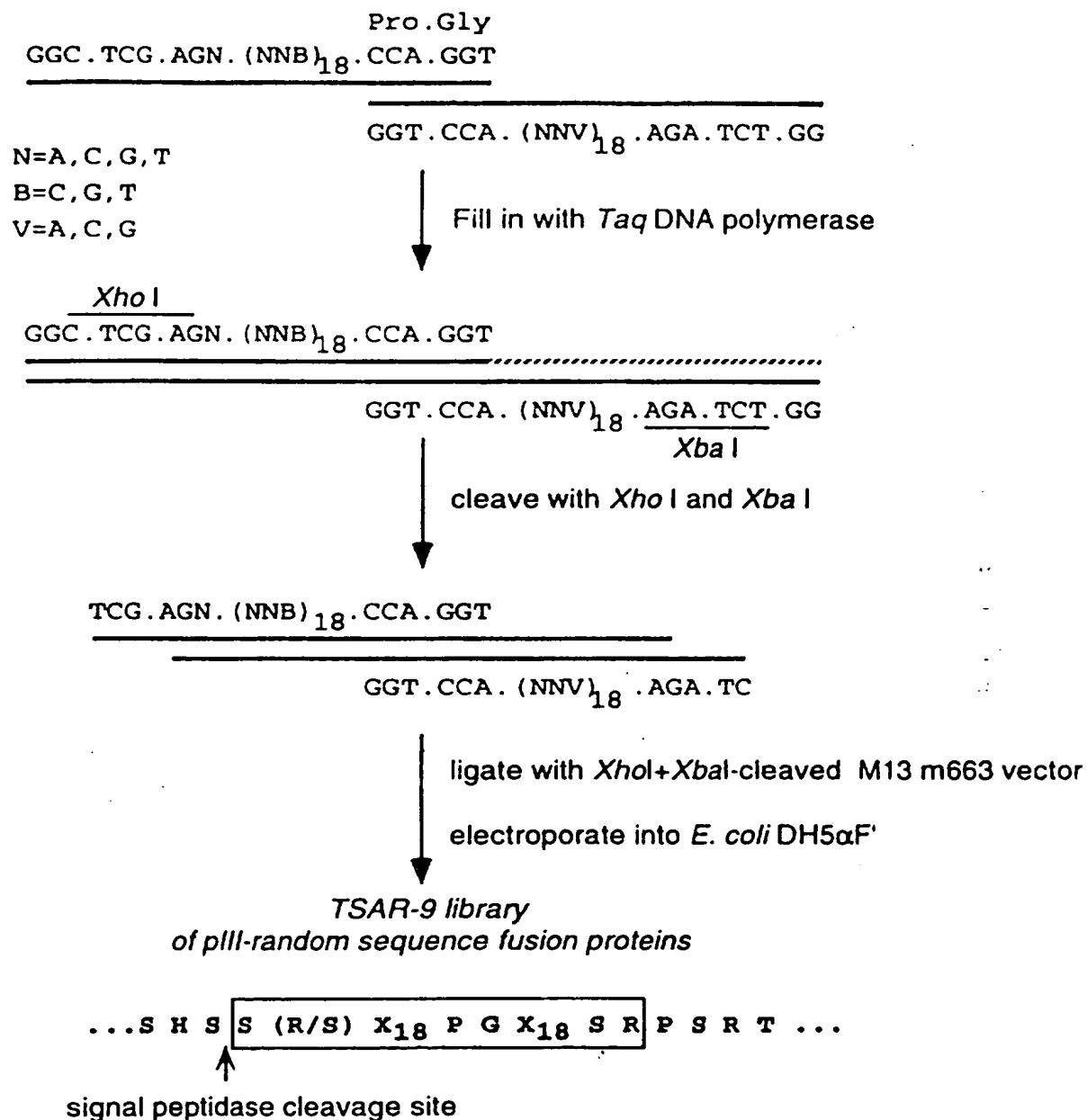
Fig. 1

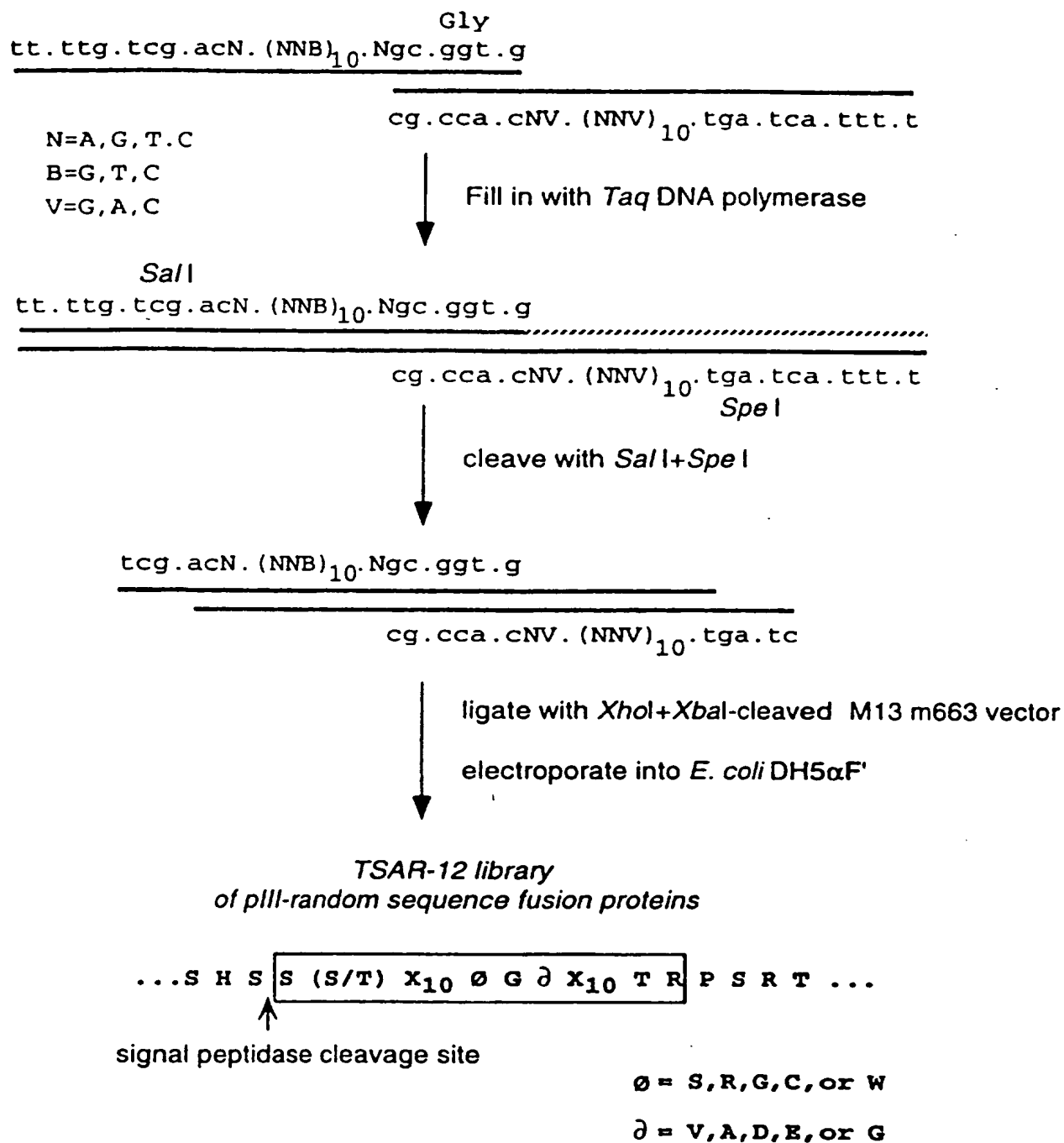
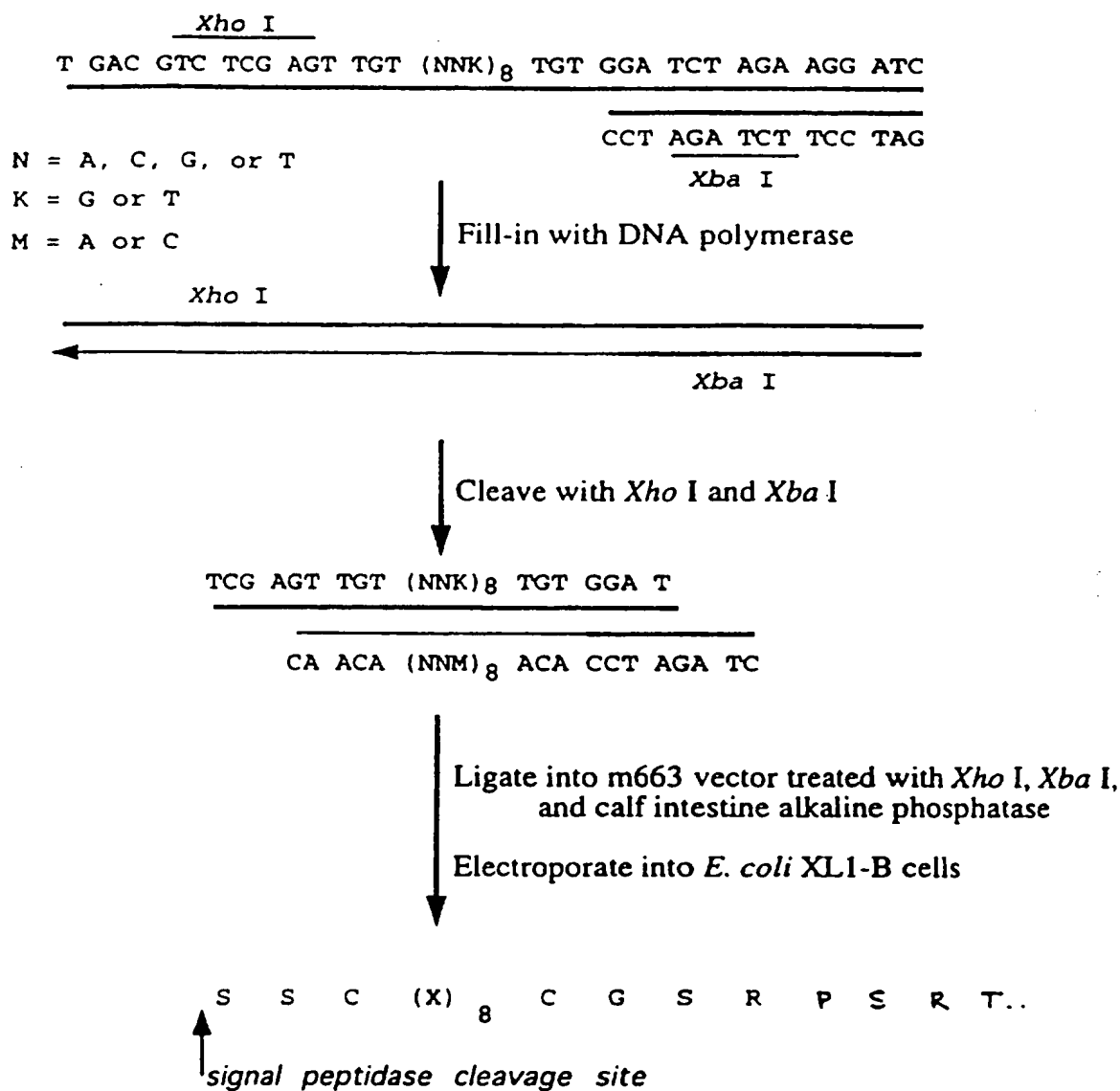
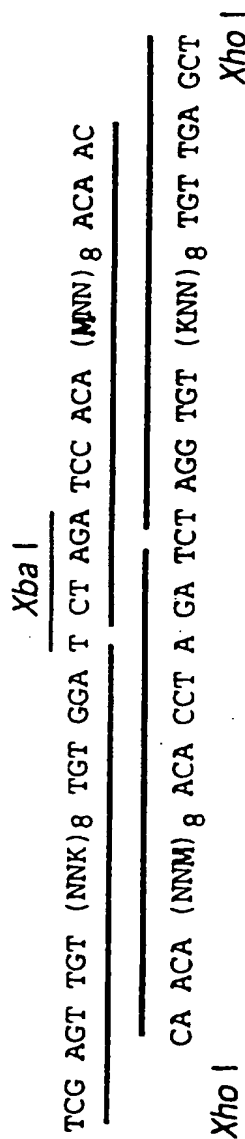
Fig. 2

Fig. 3**Construction of R8C library**

Resultant amino acid sequence expressed at the amino terminus of pIII

Fig. 4

Origin of One Class of Double-insert R8C Recombinants



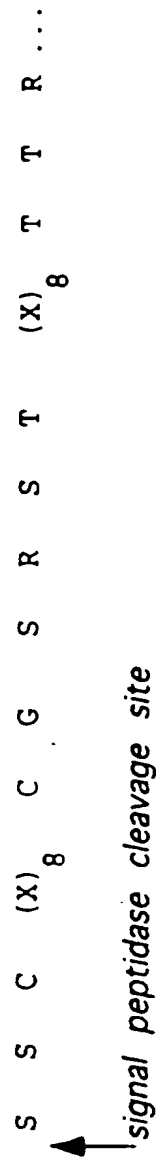
↓

Ligation of two double-stranded
oligonucleotides into a head-to-head
arrangement at the *Xba* I site

Insertion into m663 vector cleaved
by *Xho* I and *Xba* I. Illegitimate ligation
at the *Xba* I site of the vector.

↓

Electroporate into *E. coli* XL1-B cells



Resultant amino acid sequence expressed at the amino terminus of pIII

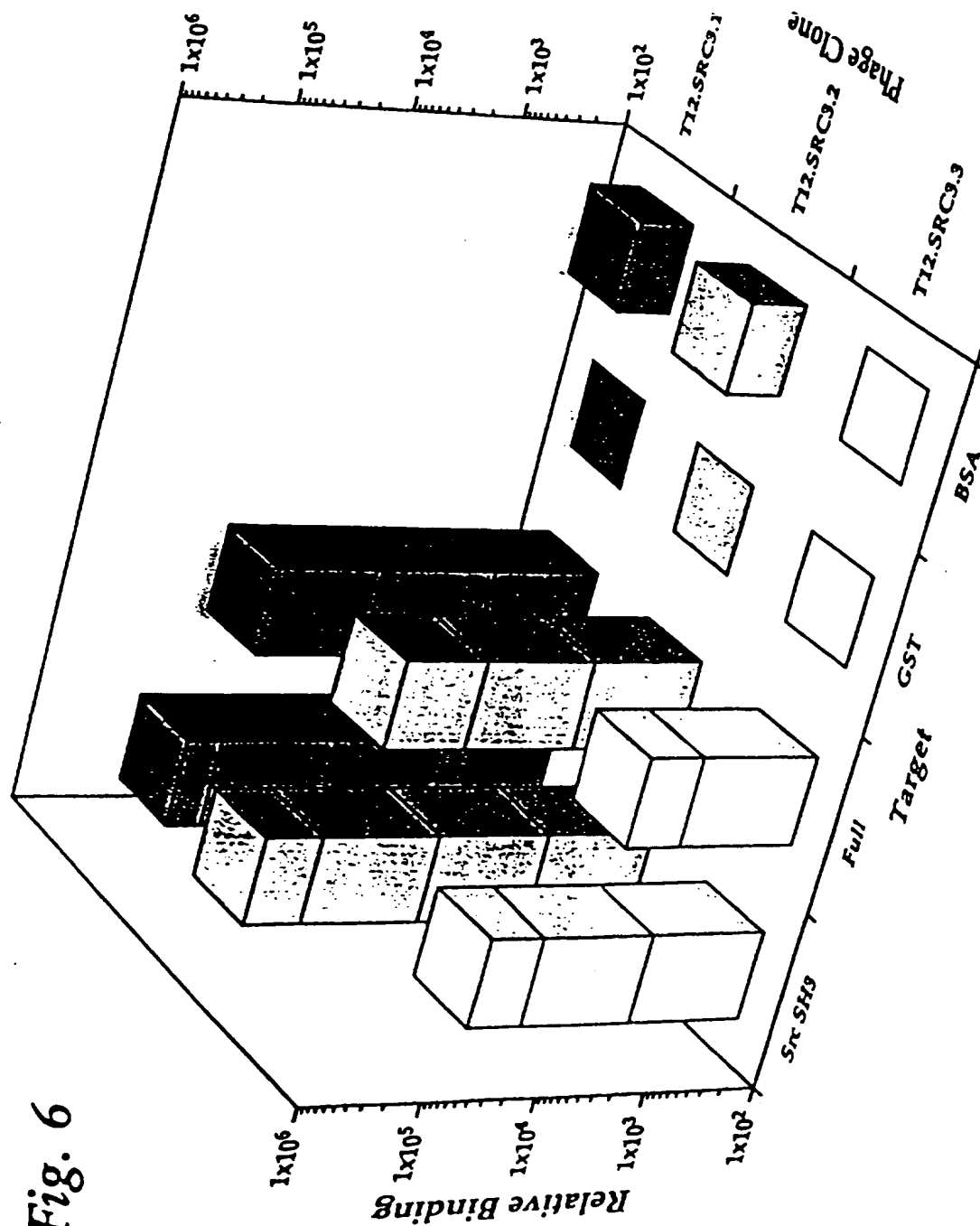
Fig. 5

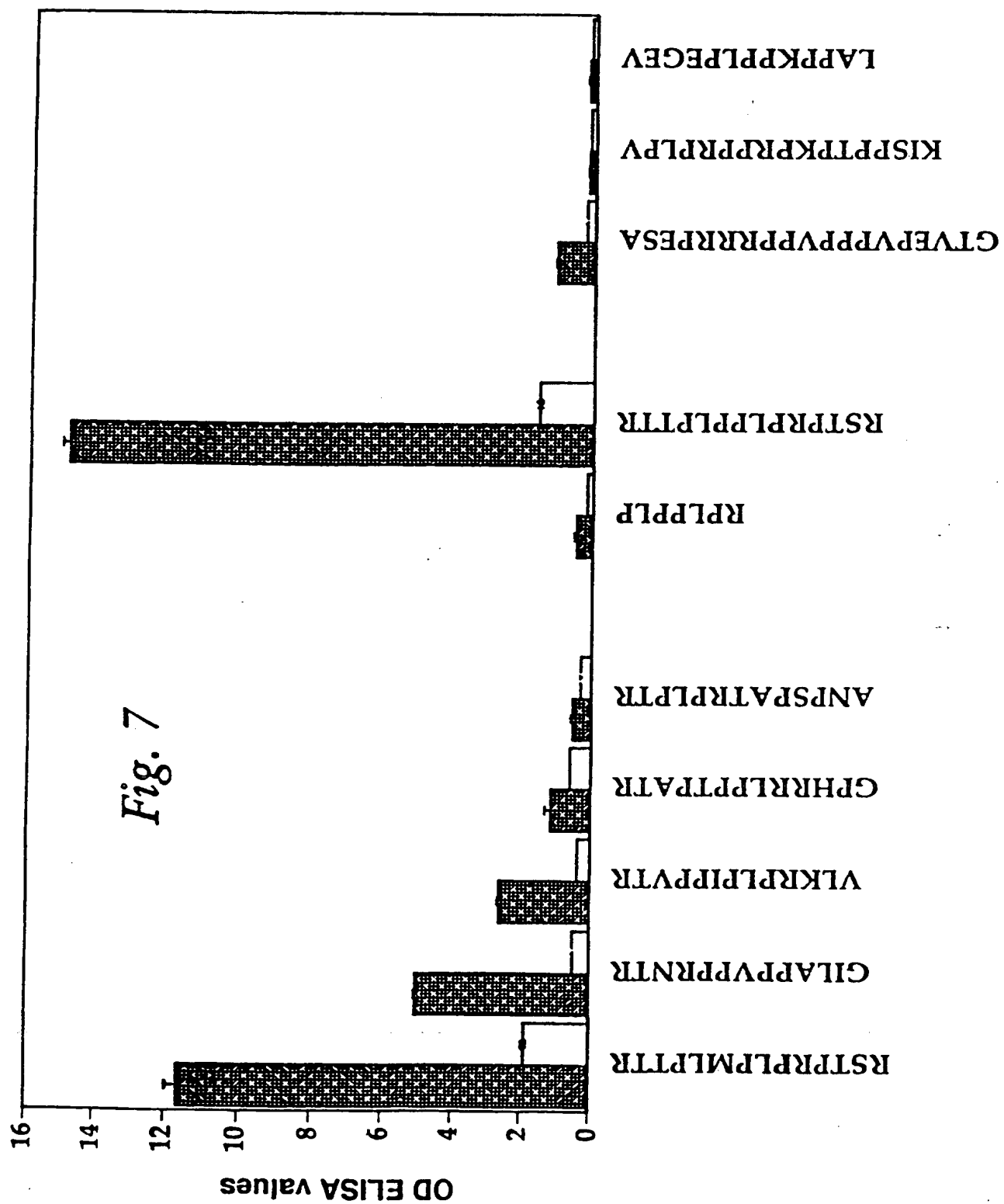
SH3 BINDING PEPTIDES FROM RANDOM PEPTIDE LIBRARIES

CLONE	SEQUENCE	FREQUENCY
T9.SRC3.2	<u>SSFDQQDWDYSIAEKMHPIRQGF</u> RELPLP <u>PSRASFGGASRPSR</u>	2
T12.SRC3.4	<u>STNVWVTGSVIARGAQS</u> RPLPIPP <u>ETRPSR</u>	1
T12.SRC3.6	<u>STAPWGLRVAHEGGVLK</u> RPLPIPP <u>VTRPSR</u>	1
T9.SRC3.4	<u>SSSGYVVPKRLGDMREYNAHGLHVPPN</u> SPLPLP <u>THLOSSRPSR</u>	1
T9.SRC3.6	<u>SSRGEENNISSRPFLSNDDPGVSNKLTGR</u> GPLPLP <u>NDSRPSR</u>	2
T12.SRC3.7	<u>STAVSFRFMPGGGAFYST</u> RPVPPI <u>TRPSR</u>	1
T12.SRC3.5	<u>STAHSLWDWGTFSGVSHKS</u> RLPLPT <u>TRPSR</u>	1
T9.SRC3.7	<u>XPGYARIVSYRF</u> RALPPP <u>SASRPSR</u>	1
T12.SRC3.3	<u>STNDVDMHMMNSGGPH</u> RRLPPT <u>ATRPSR</u>	4
T9.SRC3.5	<u>SSDNWARRVHASELIYTDLSPGILLAQ</u> RQLPPT <u>GRDPHSRPSR</u>	1
T9.SRC3.1	<u>SSSPLMYNRVGAQLTSVPGSMHFALQ</u> RRLPRT <u>PPASRPSR</u>	5
T12.SRC3.2	<u>STRWSHWPGYVGGANPSPAT</u> RPLPTR <u>SRTVESC</u>	19
T9.SRC3.3	<u>SBYNDLGTRVPSEVIKYDYFEGYSQHVITPDGSYST</u> RPLPSR <u>SRTVESC</u>	2
T9.SRC3.8	<u>XPG</u> RILLPS <u>EPRTFNYGHDSRPSR</u>	1
T12.SRC3.1	<u>STMYGVSWLSSGGGILA</u> PPVPPN <u>TRPSR</u>	25
	Consensus RLPPLP	
R8C.YES3.6	<u>SSCTEKTVSGWCGSRST</u> RPLPLP <u>RTTRPSR</u>	1
R8C.YES3.5	<u>SSCMLPTDQWQCGSRSTP</u> RPLPMLP <u>TRPSR</u>	1
R8C.YES3.3/SRC3.1	<u>SSCDGTQFRLNCGSRSTN</u> RPLPMIP <u>TRPSR</u>	3
R8C.YES3.1/SRC3.2	<u>SSCMQGGAGLKCGSRST</u> RPLPSLP <u>ITTRPSR</u>	7
R8C.YES3.7	<u>SSCYREKDTWGGGSRSTS</u> RPLPSLP <u>TRPSR</u>	2
R8C.YES3.2	<u>SSCLFEQAGTCGSRST</u> RSLPPLP <u>PTTRPSR</u>	2
R8C.YES3.4	<u>SSCDHTLGLGWCGSRST</u> RQLPIPP <u>TTTRPSR</u>	1
R8C.YES3.10	<u>SSCDTGRIAPGCGSRSTP</u> RPLPLIP <u>TTPRSTNLNSTTRPSR</u>	2
R8C.YES3.8	<u>SSCGLDNAAKTCGSRST</u> RPLPPTP <u>LTTRPSR</u>	2
R8C.YES3.9	<u>SSCSRAHETEMCGSRST</u> RPQPPP <u>ITTRPSR</u>	2
	Consensus RLPPLP	

Binding Characteristics of Src SH3-Binding Phage

Fig. 6





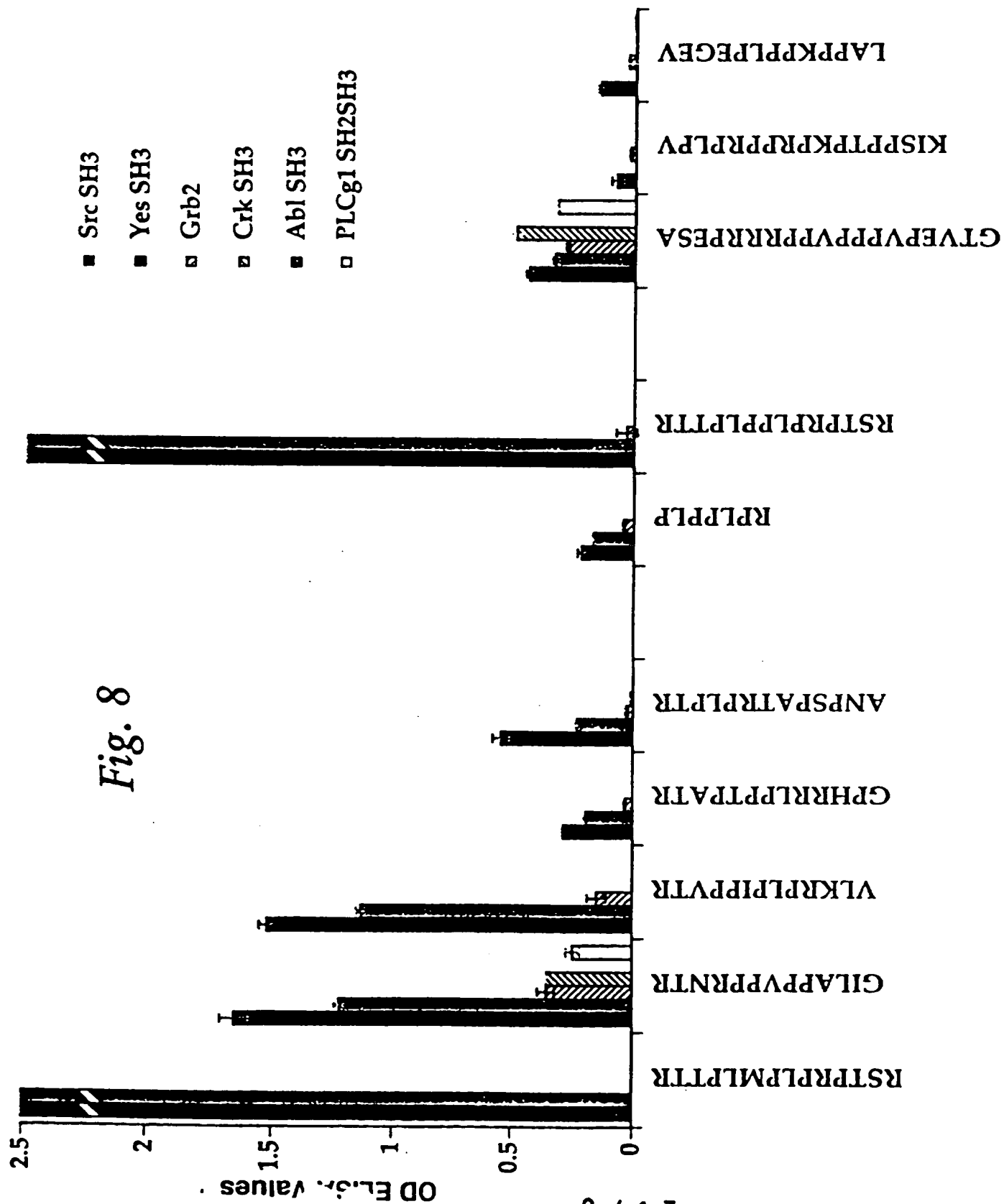
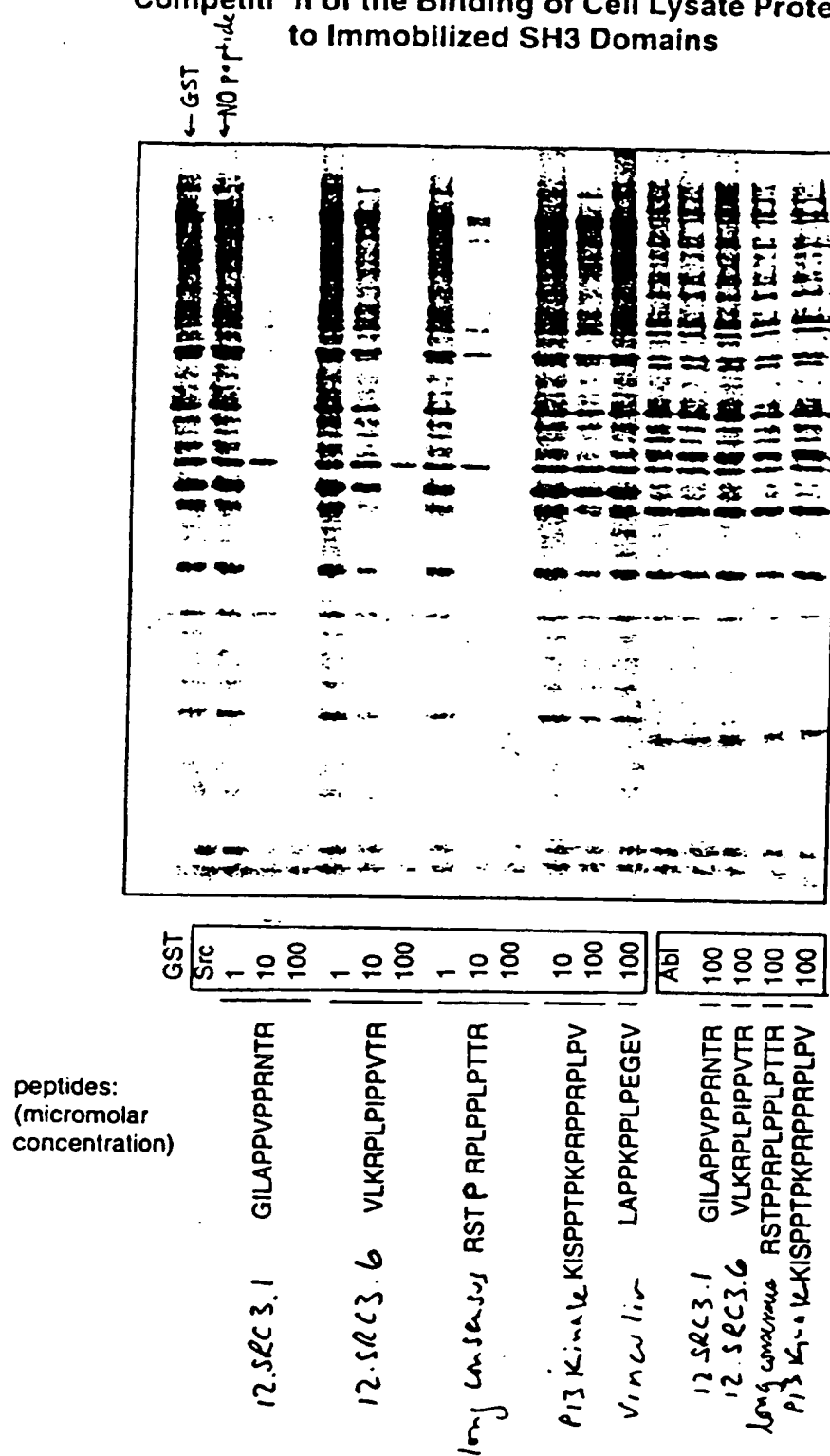


Fig. 9

Competition of the Binding of Cell Lysate Proteins to Immobilized SH3 Domains



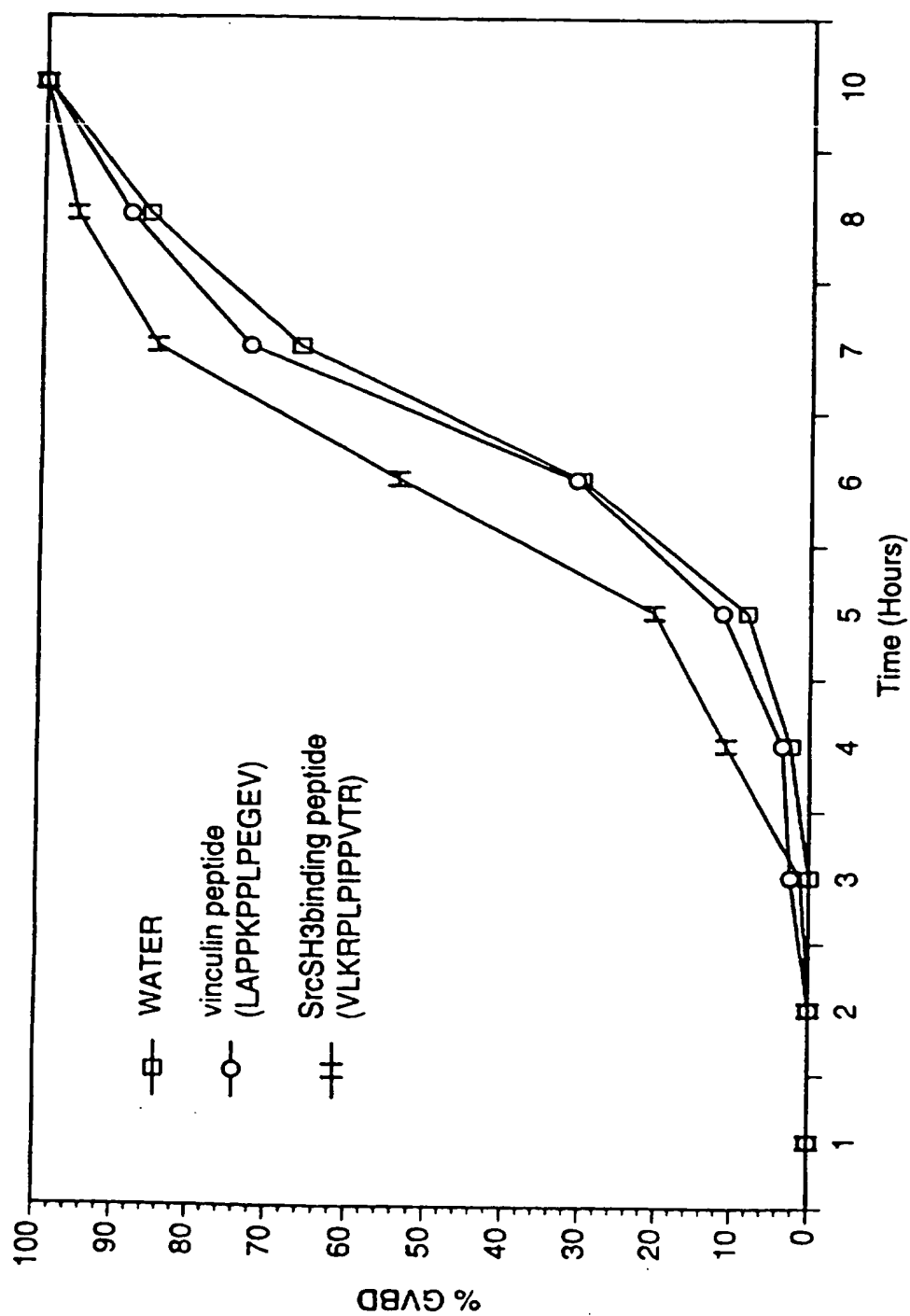


Fig. 10

Fig. 11

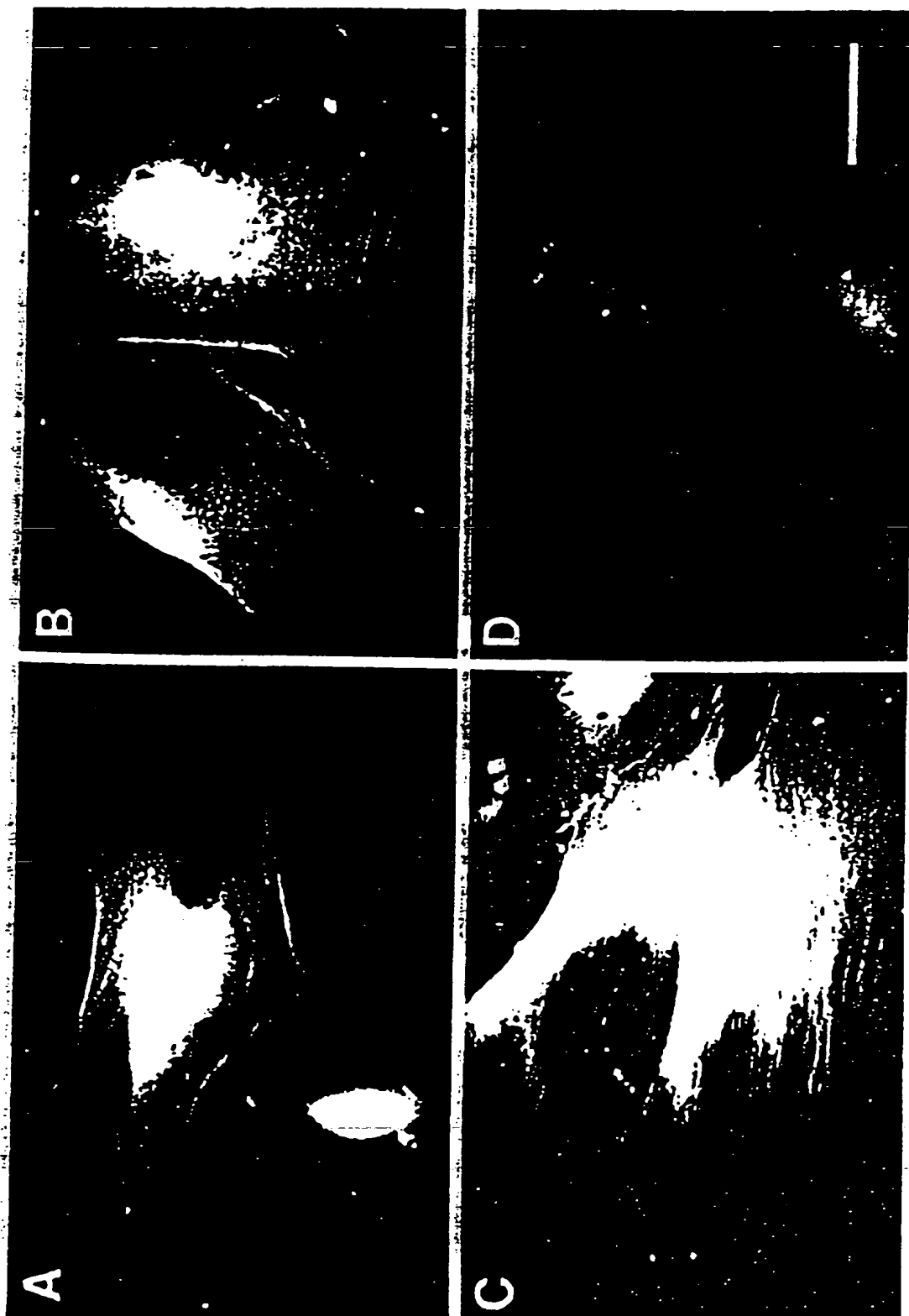


FIGURE 12

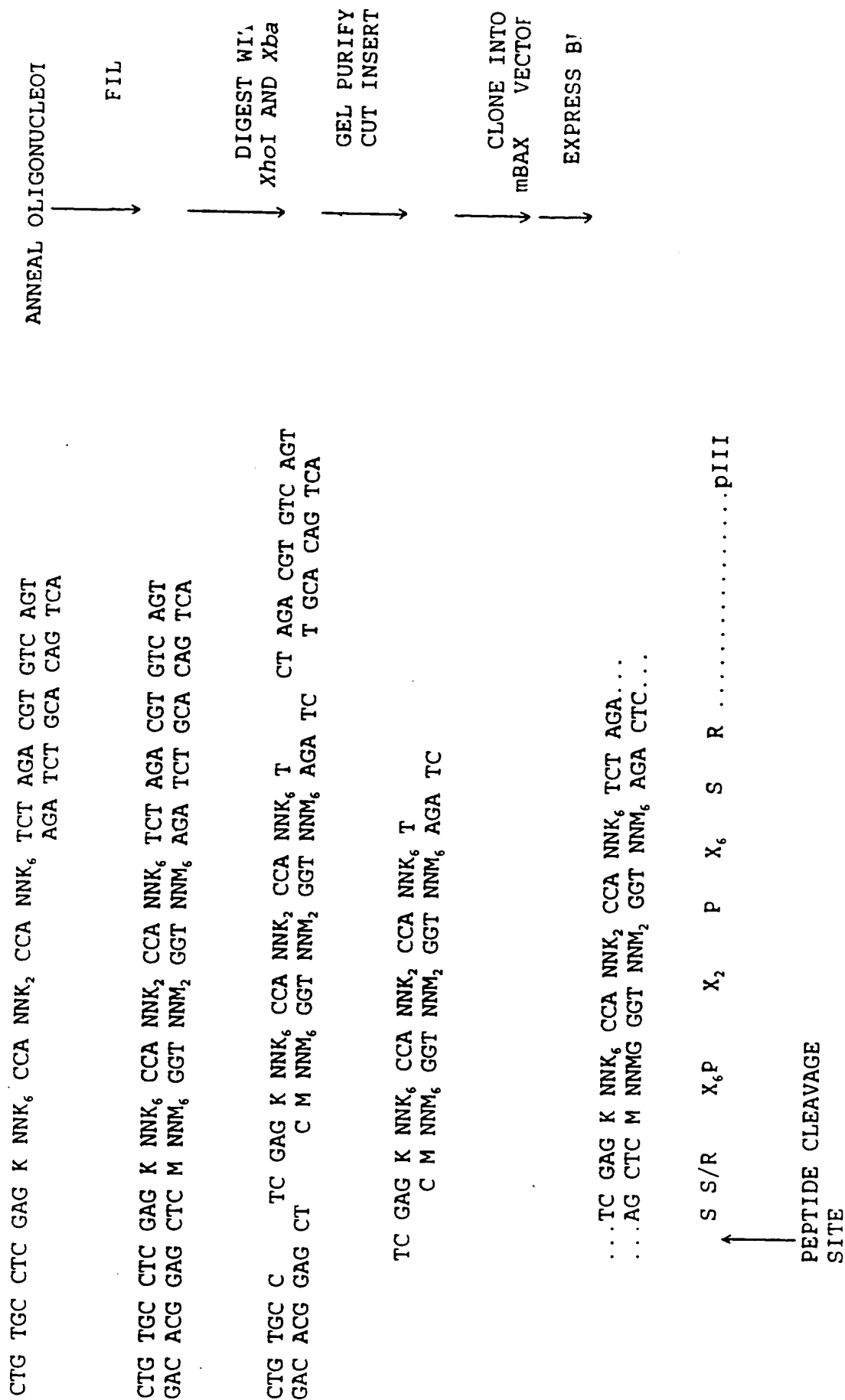
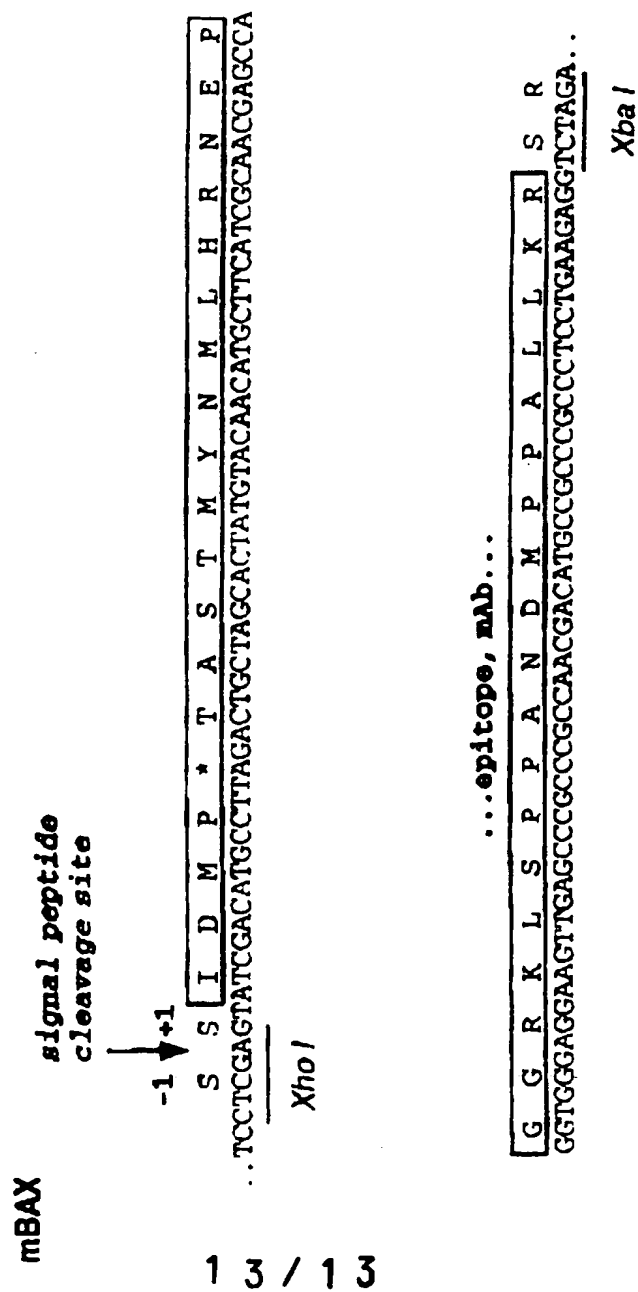


FIGURE 13



INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/09382

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : 435/5, 7.1, 172.1, 320.1; 530/300; 514/2

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/5, 7.1, 172.1, 320.1; 530/300; 514/2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG, STN

search terms: sh3, src, peptides

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P	The Journal of Biological Chemistry, Volume 269, Number 39, issued 30 September 1994, Sparks et al., "Identification and Characterization of Src SH3 Ligands from Phage-displayed Random Peptide Libraries", pages 23853-23856, see entire article.	1-74
X --- Y	Journal of the American Chemical Society, Volume 115, issued 1993, Chen et al. "Biased Combinatorial Libraries: Novel Ligands for the SH3 Domain of Phosphatidylinositol 3-Kinase", pages 12591-12592, see entire article, especially Tables I and II.	1-6, 24, 26, 28, 29, 53 ----- 7-23, 25, 27, 30-51, 53-74



Further documents are listed in the continuation of Box C.



See patent family annex.

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O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

19 OCTOBER 1995

Date of mailing of the international search report

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/09382

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Science, Volume 249, issued 28 September 1990, Langer, "New Methods of Drug Discovery", pages 1527-1533, see entire article.	51, 52, 54-57
Y	Science, Volume 257, issued 07 August 1992, Cicchetti et al., "Identification of a Protein That Binds to the SH3 Region of Abl and Is Similar to BCR and GAP-rho"; pages 803-806, see entire article.	7-23, 25, 27, 30-50
Y	Gene, Volume 128, issued 1993, Kay et al., "An M13 Phage Library Displaying Random 38-amino-acid Peptides as a Source of Novel Sequences with Affinity to Selected Targets", pages 59-65, see entire article.	7-23, 25, 27, 30-48, 61-68

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US95/09382

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

G01N 33/53; C12Q 1/70; C12N 5/10. 7/01; C07K 7/00, 14/00; A61K 38/03



INTERNATIONAL APPLICATION PUBLISHED UNDER

WO 9603649A1

(51) International Patent Classification ⁶ : G01N 33/53, C12Q 1/70, C12N 5/10, 7/01, C07K 7/00, 14/00, A61K 38/03		A1	(11) International Publication Number: WO 96/03649
			(43) International Publication Date: 8 February 1996 (08.02.96)
(21) International Application Number: PCT/US95/09382		(81) Designated States: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, MW, SD, SZ, UG).	
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(30) Priority Data: 278,865 22 July 1994 (22.07.94) US 483,555 7 June 1995 (07.06.95) US			
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(74) Agents: MISROCK, S., Leslie et al.; Pennie & Edmonds, 1155 Avenue of the Americas, New York, NY 10036 (US).			
(54) Title: Src SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME			
(57) Abstract			
<p>Peptides having general and specific binding affinities for the Src homology region 3 (SH3) domains of proteins are disclosed in the present invention. In particular, SH3 binding peptides have been isolated from three phage-displayed random peptide libraries which had been screened for isolates that bind to bacterial fusion proteins comprising SH3 and glutathione S-transferase (GST). Preferred peptides are disclosed which comprise a core 7-mer sequence (preferably, a consensus motif) and two or more, preferably at least six, additional amino acid residues flanking the core sequence, for a total length of 9, preferably at least 13, amino acid residues and no more than about 45 amino acid residues. Such peptides manifest preferential binding affinities for certain SH3 domains. The preferred peptides exhibit specific binding affinities for the Src-family of proteins. <i>In vitro</i> and <i>in vivo</i> results are presented which demonstrate the biochemical activity of such peptides.</p>			

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**Src SH3 BINDING PEPTIDES AND
METHODS OF ISOLATING AND USING SAME**

1. Field of the Invention

5 The present invention relates to SH3 binding peptides having a broad range of binding specificities. That is, certain members of the SH3 binding peptides disclosed bind with approximately the same facility with SH3 domains derived from different SH3 domain-containing proteins. Other
10 members, in contrast, bind with a much greater degree of affinity for specific SH3 domains. The SH3 binding peptides are obtained from random peptide libraries that are also phage-displayed. Methods are described of obtaining the phage clones that bind to the SH3 domain targets and of
15 determining their relevant nucleotide sequences and consequent primary amino acid sequence of the binding peptides. The resulting SH3 binding proteins are useful in a number of ways, including, but not limited to, providing a method of modulating signal transduction pathways at the
20 cellular level, of modulating oncogenic protein activity or of providing lead compounds for development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction.

25 2. Background of the Invention

2.1. Src and the SH3 Domain

 Among a number of proteins involved in eukaryotic cell signaling, there is a common sequence motif called the SH3 domain. It is 50-70 amino acids in length,
30 moderately conserved in primary structure, and can be present from one to several times in a large number of proteins involved in signal transduction and in cytoskeletal proteins.

 The protein pp60c-src represents a family of at least nine non-receptor protein tyrosine kinases (NR-PTKs).
35 Members of this family share an overall structural organization comprising a series of catalytic and non-catalytic domains. In Src, a 14-amino-acid myristylation

signal resides at the extr me amino-terminus, and is followed by a unique region that is not highly conserved among family members. Following this r gion are two highly conserved 60- and 100-amino-acid regions, the Src homology (SH) domains 3 and 2, respectively. SH2 and SH3 domains have been shown to play an important role in mediating protein-protein interactions in a variety of signaling pathways. Koch, C.A., et al., in Science (1991) 252:668-74. The carboxy-terminal half of Src contains the PTK catalytic domain, as well as a negative regulatory tyrosine (Y527) near the carboxy terminus. Phosphorylation of this residue (e.g., by Csk) results in the inhibition of PTK activity. Cooper, J.A., et al., in Science (1986) 231:1431-1434. Mutation of Y527->F generates forms of Src with increased PTK and oncogenic activity. Cartwright, C.A., et al., in Cell (1987) 49:83-91; Kmiecik, T.E., et al., in Cell (1987) 49:65-73; and Piwicna-Worms, H., et al., in Cell (1987) 75-82.

The fact that some mutations which result in increased Src PTK and transforming activity map to the Src SH2 (Seidel-Dugan, C., et al., in Mol. Cell. Biol. (1992) 12:1835-45; and Hirai, H. and Varmus, H.E. in Mol. Cell. Biol. (1990) 10:1307-1318) and SH3 domains (Seidel-Dugan, C., et al., supra; Hirai, H. and Varmus, H.E., supra; Superti-Furga, G., et al., in Embo. J. (1993) 12:2625-34; and Potts, W.M., et al., in Oncogene Res. (1988) 3:343-355) suggests a negative regulatory role for these domains. That phosphotyrosine residues within specific sequence contexts represent high affinity ligands for SH2 domains suggests a model in which the SH2 domain participates in Y527-mediated inhibition of PTK activity by binding phosphorylated Y527, thereby locking the kinase domain in an inactive configuration. Matsuda, M., Mayer, B.J., et al., in Science (1990) 248:1537-1539. This model is supported by the observation that phosphopeptides corresponding to the carboxy-terminal tail of Src bind active, but not inactive, variants of Src. Roussel, R.R., et al., in Proc. Natl. Acad. Sci. U S A (1991) 88:10696-700; and Liu, X., et al., in Oncogen (1993) 8:1119-1126.

The mechanism of SH3-mediated inhibition of Src PTK activity remains unclear. There is evidence that pY527-mediated inhibition of Src PTK activity involves the SH3 domain as well as the SH2 domain. Okada, M., Howell, et al., in J. Biol. Chem. (1993) 268:18070-5; Murphy, S.M., et al., in Mol. Cell. Biol. (1993) 13:5290-300; and Superti-Furga, G., et al., *supra*. Although these effects are thought to be a consequence of SH3-mediated protein-protein interactions, precisely how the Src SH3 domain exerts its negative regulatory effect is unclear. Identification of high affinity ligands for the Src SH3 domain could help resolve these issues.

2.2. Protein Tyrosine Kinases and The Immune Response

Src-related tyrosine kinases are expressed in a variety of cell types including those of the immune system (lymphocytes, T cells, B cells, and natural killer cells) and the central nervous system (neural cells, neurons, oligodendrocytes, parts of the cerebellum, and the like). Umemori, H. et al., in Brain Res. Mol. Brain Res. (1992) Dec. 16(3-4):303-310. Their presence in these cells and tissues and their interaction with specific cell surface receptors and immunomodulatory proteins (such as T cell antigen receptor, CD14, CD2, CD4, CD40 or CD45) suggest that these kinases serve an important role in the signalling pathways of not only the central nervous system but of the immune system, as well. See, e.g., Ren, C.L. et al., in J. Exp. Med. (1994) 179(2):673-680 (signal transduction via CD40 involves activation of Lyn kinase); Donovan, J.A. and Koretzky, G.A., in J. Am. Soc. Nephrol. (1993) 4(4):976-985 (CD45, the immune response, and regulation of Lck and Fyn kinases); and Carmo, A.M. et al., in Eur. J. Immunol. (1993) 23(9):2196-2201 (physical association of the cytoplasmic domain of CD2 with p56lck and p59fyn).

For instance, mice with disruptions in their Src-like genes, Hck and Fgr, possess macrophages with impaired phagocytic activity or exhibit a novel immunodeficiency

characterized by an increased susceptibility to infection with *Listeria monocytogenes*. Lowell, C.A. et al., in Genes Dev. (1994) 8(4):387-398. Also, it has been shown that bacterial lipopolysaccharide (LPS) activates CD14-associated p56lyn, p68hck, and p59c-fgr, while inducing the production of lymphokines, such as TNF-alpha, IL-1, IL-6, and IL-8. Inhibition of the protein tyrosine kinases blocks production of TNF-alpha and IL-1.

10 2.3. SH3 Binding Peptides

As mentioned above, it has long been suspected that SH3 domains are sites of protein-protein interaction, but it has been unclear what SH3 domains actually bind. Efforts to identify ligands for SH3 domains have led to the characterization of a number of SH3-binding proteins, including 3BP1 and 2 (Ren, R., Mayer, et al., in Science (1993) 259:1157-61), SOS (Olivier, J.P., et al., in Cell (1993) 73:179-91; and Rozakis-Adcock, M., et al., in Nature (1993) 363:83-5), p85 PI-3' Kinase (Xingquan, L., et al., in Mol. Cell. Biol. (1993) 13:5225-5232), dynamin (Gout, I., et al., in Cell (1993) 75:25-36), AFAP-110 (Flynn, D.C., et al., in Mol. Cell. Biol. (1993) 13:7892-7900), and CD42 (Barford, E.T., et al., in J. Biol. Chem. (1993) 268:26059-26062). These proteins tend to possess short, proline-rich stretches of amino acids, some of which have been directly implicated in SH3 binding. A variety of consensus sequences have been proposed, although the similarity among proline-rich regions of different SH3-binding proteins tends to be fairly low. Also, attempts to build consensus sequences are likely complicated by the incorporation of data from proteins that bind different SH3 domains.

Thus, Cicchetti, P., et al., in Science (1992) 257:803-806, published their work relating to the isolation and sequencing of two naturally-occurring proteins that could be bound *in vitro* by the SH3 domain of the *abl* oncogene product. These workers found that SH3 domains bind short, proline-rich regions of such proteins. Subsequently, this same group

disclosed further results (Ren, R. et al., supra) in which the SH3 binding sites of the SH3 binding proteins were localized to "a nine- or ten-amino acid stretch rich in proline residues." A consensus sequence incorporating the features of the SH3 binding sites of four SH3 binding proteins was proposed: XPXXPPP*XP (SEQ ID NO:1), wherein X indicates a position in the amino acid sequence which is not conserved among the four SH3 binding proteins, P represents proline, and * indicates a hydrophobic amino acid residue, such as P or L.

The screening of complex random peptide libraries has been used to identify peptide epitopes for monoclonal (Scott, J.K. and Smith, G.P. in Science (1990) 249:386-390) and polyclonal (Kay, B.K., et al., in Gene (1993) 128:59-65) antibodies, as well as peptide ligands for a variety of proteins, including streptavidin (Devlin, J.J., et al., in Science (1990) 249:404-406; and Lam, K., et al., in Nature (1991) 354:82-84), the endoplasmic reticulum chaperone BiP (Blond-Elguindi, S., et al., in Cell (1993) 75:717-728), and CaM (Dedman, J.R., et al., in J. Biol. Chem. (1993) 268:23025-23030).

Recently, Chen, J.K. et al., in J. Am. Chem. Soc. (1993) 115:12591-12592, described ligands for the SH3 domain of phosphatidylinositol 3-kinase (PI-3' Kinase) which were isolated from a biased combinatorial library. A "biased" library is to be distinguished from a "random" library in that the amino acid residue at certain positions of the synthetic peptide are fixed, i.e., not allowed to vary in a random fashion. Indeed, as stated by these research workers, screening of a "random" combinatorial library failed to yield suitable ligands for a PI-3' Kinase SH3 domain probe. The binding affinities of these unsuitable ligands was described as weak, >100 μ M, based on dissociation constants measured by the Biosensor System (BIAcore).

35

More recently, Yu, et al. (Yu, H., et al., in Cell (1994) 76:933-945) used a "biased" synthetic peptide library

of the form XXXPPXPXX (SEQ ID NO:2), wherein X represents any amino acid other than cysteine, to identify a series of peptides which bind the Src and PI-3' Kinase SH3 domains. The bias was accomplished by fixing the proline residues at 5 the specific amino acid positions indicated for the "random" peptide. As stated previously, without this bias, the technique disclosed fails to identify any SH3 domain-binding peptides.

A consensus sequence, based on 13 binding peptides was 10 suggested: RXLPPRPXX (SEQ ID NO:3), where X tends to be a basic residue (like R, K or H). The binding affinities of several SH3 binding peptides were disclosed as ranging from 8.7 to 30 μ M. A "composite" peptide, RKLPPRRR (SEQ ID NO:4), was reported to have a binding affinity of 7.6 μ M. 15 This value compares favorably to the binding affinity of the peptide, VPPPVPPIRRR (SEQ ID NO:5), to the N-terminal SH3 domain of Grb2. See, Kraulis, P.J. J. Appl. Crystallogr. (1991) 24:946. Recognizing the limitations of their technique, Chen and co-workers, *supra*, stated that their 20 results "illustrate the utility of biased combinatorial libraries for ligand discovery in systems where there is some general knowledge of the ligand-binding characteristics of the receptor" (emphasis added).

Yu and co-workers, *supra*, further described an SH3 25 binding site consensus sequence, XpØPpXP (SEQ ID NO:6), wherein X represents non-conserved residues, Ø represents hydrophobic residues, P is proline, and p represents residues that tend to be proline. A consensus motif of RXLPPRPXX (SEQ ID NO:7), where X represents any amino acid other than 30 cysteine, was proposed for ligands of PI-3' Kinase SH3 domain. A consensus motif of RXLPPLPRØ (SEQ ID NO:8), where Ø represents hydrophobic residues, was proposed for ligands of Src SH3 domain. Still, the dissociation constants reported for the 9-mer peptides ranged only from about 8-70 35 μ M and selectivity between one type of SH3 domain and another was relatively poor, the K_D s differing by only about a factor of four.

Hence, there remains a need to develop techniques for the identification of Src SH3 binding peptides which do not rely on such "biased" combinatorial peptide libraries that are limited to a partially predetermined set of amino acid sequences. Indeed, the isolation of SH3 binding peptides from a "random" peptide library has not been achieved successfully before now. Furthermore, particular peptides having much greater binding affinities, whether general or more selective binding for specific SH3 domains, remain to be identified. Binding peptides specific for particular SH3 domains are useful, for example, in modulating the activity of a particular SH3 domain-containing protein, while leaving others bearing an SH3 domain unaffected. Still, the more promiscuous general binding peptides are useful for the modulation of a broad spectrum of SH3 domain-containing proteins.

The present invention relates to such SH3 binding peptides, methods for their identification, and compositions comprising same. In particular, peptides comprising particular sequences of amino acid residues are disclosed which were isolated from random peptide libraries. In the present invention, clones were isolated from a phage-displayed random peptide library which exhibited strong binding affinities for SH3 domain-containing protein targets. Some of these protein targets, include Abl, Src, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, and p85 PI-3' Kinase. From the nucleotide sequence of the binding phage, the amino acid sequence of the peptide inserts has been deduced. Synthetic peptides having the desired amino acid sequences are shown to bind the SH3 domain of the target proteins. In particular, synthetic peptides combining a core consensus sequence and additional amino acid residues flanking the core sequence are especially effective at binding to particular target protein SH3 domains. The SH3 binding peptides disclosed herein can be utilized in a number of ways, including the potential modulation of oncogenic protein activity in vivo. These peptides also serve as useful leads in the production of

peptidomimetic drugs that modulate a large class of proteins involved in signal transduction pathways and oncogenesis.

3. Summary of the Invention

5 Accordingly, three phage-displayed random peptide libraries were screened for isolates that bind to bacterial fusion proteins consisting of the Src homology region 3 (SH3) and glutathione S-transferase (GST). DNA sequencing of the isolates showed that they contained sequences that resemble
10 the consensus motif, RPLPPLP (SEQ ID NO:9), within their 8, 22, or 36 amino acid long random regions. When peptides were synthesized corresponding to the pIII inserts of the SH3-binding phage, they bound to the GST fusions of the SH3 domains of Src and the Src-related proteins, such as Yes, but
15 not of Grb2, Crk, Abl, or PLC γ 1. The synthesized peptides bind quite well to the Src SH3 domain and act as potent competitors of natural Src SH3 interactions in cell lysates. For instance, these peptides can compete with radiolabelled proteins from cell lysates in binding to immobilized Src-GST,
20 with an apparent IC₅₀ of 1-10 μ M. When a peptide, bearing the consensus sequence RPLPPLP (SEQ ID NO:9) was injected into *Xenopus laevis* oocytes, it accelerated the rate of progesterone-induced maturation. These results demonstrate the utility of phage-displayed random peptide libraries in
25 identifying SH3-binding peptide sequences and that such identified peptides exhibit both *in vivo* and *in vitro* biological activity.

Thus, it is an object of the present invention to provide peptides having at least nine and up to forty-five
30 amino acid residues, including an amino acid sequence of the formula, R-2-L-P-5-6-P-8-9 (SEQ ID NO:10), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 2 represents any amino acid residue except cysteine, 5 and 6 each represents a
35 hydrophobic amino acid residue, 8 represents any amino acid residue except cysteine, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard

one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src, provided that said peptide is not R-P-L-P-P-L-P-T-S (SEQ ID NO:11). In a particular embodiment of the present invention, the peptides also exhibit a binding affinity for the SH3 domain of Src-related proteins, including Yes, Fyn, Lyn, Lck, Hck and Fgr.

The present invention also contemplates SH3 domain-binding peptides that further comprise a C-terminal-flanking amino acid sequence of the formula 10, 10-11, 10-11-12, 10-11-12-13 (SEQ ID NO:12) or 10-11-12-13-14 (SEQ ID NO:13), in which each number represents any amino acid residue except cysteine, such that 10 is bound to 9 by a peptide bond. Furthermore, peptides are also provided which further comprise an N-terminal-flanking amino acid sequence of the formula 1', 2'-1', 3'-2'-1' or 4'-3'-2'-1' (SEQ ID NO:14) in which each number represents any amino acid residue except cysteine, such that 1' is bound to R by a peptide bond.

Thus, in a particular embodiment, a peptide is disclosed having at least thirteen and up to forty-five amino acid residues, including an amino acid sequence of the formula, 3'-2'-1'-R-2-L-P-5-6-P-8-9-10 (SEQ ID NO:15), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 3', 2', 1', 2, 8, and 10 each represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src.

The present invention also seeks to provide new consensus sequences or motifs that reflect variations in SH3 domain binding selectivities or specificities. The present invention also contemplates conjugates of the SH3 binding peptides and a second molecule or chemical moiety. This second molecule may be any desired substance whose delivery to the region of the SH3 domain of a particular protein (or

cell containing the protein) is sought. Possible target cells include, but are not limited to, neural cells, immune cells (e.g., T cells, B cells, natural killer cells, and the like), osteoclasts, platelets, epidermal cells, and the like, which cells express Src, Src-related proteins, and potentially, other SH3 domain-containing proteins. In this manner, the modulation of the biological activity of proteins bearing an SH3 domain can be accomplished.

Other methods and compositions consistent with the objectives of the present invention are likewise disclosed. In particular, a method is disclosed of modulating the activity of Src or Src-related proteins comprising administering a composition comprising an effective amount of a peptide of the present invention and a carrier, preferably a pharmaceutically acceptable carrier. In a specific embodiment, the contemplated method results in the inhibition of the activity of Src or Src-related proteins. Alternatively, the method is effective to activate Src or Src-related proteins.

In yet another embodiment, a method is disclosed of identifying a peptide having a region that binds to an SH3 domain comprising: (a) providing an immobilized target protein comprising an SH3 domain; (b) incubating the immobilized target protein with an aliquot taken from a random peptide library; (c) washing unbound library peptides from the immobilized target protein; (d) recovering the peptide bound to the immobilized target protein; and (e) determining the primary sequence of the SH3 domain-binding peptide.

Moreover, a method is disclosed of imaging cells, tissues, and organs in which Src or Src-related proteins are expressed, which comprises administering an effective amount of a composition comprising an SH3 domain-binding peptide conjugated to detectable label or an imaging agent.

Other objectives of the present invention will become apparent to one of ordinary skill in the art after

consideration of the above disclosure and the following detailed description of the preferred embodiments.

4. Brief Description of the Figures

5 FIG. 1 illustrates a scheme for the generation of a random 36 amino acid peptide library (TSAR-9; e.g., SEQ ID NO:16). Oligonucleotides were synthesized (SEQ ID NOS:17-18), converted into double-stranded DNA, cleaved with restriction enzymes (SEQ ID NOS:19-20), and cloned into the
10 M13 vector, m663. The random peptide region encoded by the oligonucleotides is shown in the box (SEQ ID NO:16) and is situated at the N-terminus of mature protein III (SEQ ID NO:21).

FIG. 2 illustrates a scheme for the generation of a
15 random 22 amino acid peptide library (TSAR-12; e.g., SEQ ID NO:23). Oligonucleotides were synthesized (SEQ ID NOS:24-25), converted into double-stranded DNA, cleaved with restriction enzymes (SEQ ID NOS:26-27), and cloned into the M13 vector, m663. The random peptide region encoded by the
20 oligonucleotides is shown in the box (SEQ ID NO:23) and is situated at the N-terminus of mature protein III (SEQ ID NO:28).

FIG. 3 illustrates a scheme for the generation of a random 8 amino acid peptide library (R8C; SEQ ID NO:30).
25 Oligonucleotides were synthesized (SEQ ID NOS:31-32), converted into double-stranded DNA, cleaved with restriction enzymes (SEQ ID NOS:33-34), and cloned into the M13 vector, m663. The random peptide region (SEQ ID NO:30) is flanked by cysteine residues and is situated at the N-terminus of mature
30 protein III (SEQ ID NO:35).

FIG. 4 illustrates the possible origin of one class of double-insert R8C recombinants (e.g., encoding SEQ ID NO:36). Double-stranded oligonucleotides (e.g., SEQ ID NO:37) may have ligated in a head-to-head fashion at the Xba I site
35 prior to cloning in the Xho I- Xba I cleaved M13 vector.

FIG. 5 shows a list of random peptide recombinants (SEQ ID NOS:38-61 and 106) isolated by the method of the present

invention and the displayed peptide sequence. The amino acid sequences are aligned to highlight the core sequences. The flanking sequences are shown to the N-terminal and C-terminal ends of the core sequence.

5 FIG. 6 graphically illustrates the relative binding affinities of selected phage clones for various SH3 domains. The results indicate that certain amino acid sequences provide generic SH3 domain binding, while others can provide greater selectivity for the SH3 domain of Src. Still other
10 clones exhibit Src SH3 domain preferential binding.

FIG. 7 shows the binding of synthetic peptides (SEQ ID NOS:9 and 62-70) representing Src SH3-selected phage inserts to Src SH3-GST fusion target (shaded columns) over background GST binding (unshaded columns) relative to the core peptide
15 RPLPPLP (SEQ ID NO:9) and proline-rich peptide segments derived from naturally occurring proteins. Bound biotinylated peptide was detected with streptavidin-alkaline phosphatase ELISA. Each point was performed in triplicate; average absorbance at 405 nm is presented. Error bars
20 represent SD.

FIG. 8 illustrates the relative specificity of selected peptides (SEQ ID NOS:9 and 62-70) for SH3 domains derived from different proteins. In particular, the binding affinities of the peptides for the SH3 domains of the
25 following protein fusion targets were tested: Src SH3-GST, Yes SH3-GST, Grb2-GST, Crk SH3-GST, Abl SH3-GST, PLC γ 1 SH2SH3-GST. Bound biotinylated peptide was detected with streptavidin-alkaline phosphatase. Each point was performed in triplicate; values are average signal (absorbance at 405
30 nm) above GST background, with error bars representing standard deviation. Hatched bars indicate saturation of the ELISA signal.

FIG. 9 presents the results of competition experiments in which selected peptides were found to inhibit the binding
35 of proteins from cell lysates to immobilized Src SH3-GST or Abl SH3-GST protein in fusion targets.

FIG. 10 presents a graph illustrating the increased rate of progesterone-induced maturation of oocytes injected with an SH3 domain-binding peptide, VLKRPLPIPPVTR (SEQ ID NO:64), of the present invention. Briefly, Stage VI oocytes were prepared and injected as previously described (see, Kay, B.K., in Methods in Cell Biol. (1991) 36:663-669). Oocytes were injected with 40 nL of 100 μ M test peptide or water. After injection, the oocytes were placed in 2 μ g/mL progesterone (Sigma, St. Louis, MO) and scored hourly for germinal vesicle breakdown (GVBD).

FIG. 11 shows the results of fluorescence experiments in which certain peptides, Panel A = VLKRPLPIPPVTR (SEQ ID NO:64), Panel B = GILAPPVPPRNTR (SEQ ID NO:63), Panel C = RSTPRPLPPLPTTR (SEQ ID NO:67), of the invention were shown to localize within cellular compartments thought to contain Src or Src-related proteins.

FIG. 12 illustrates a scheme for the generation of a biased peptide library. Oligonucleotides were synthesized, converted into double-stranded DNA, cleaved with restriction enzymes XhoI and XbaI, and cloned into the mBAX vector, described further below in the Examples section. The biased peptide region is situated at the N-terminus of mature pIII protein.

FIG. 13 illustrates the peptide sequence encoded in the mBAX vector situated at the N-terminus of mature pIII protein.

5. Detailed Description of the Preferred Embodiments

5.1. General Considerations

The present invention relates to peptides that exhibit a binding affinity for an SH3 domain, which domain has been found to be present in a number of physiologically significant proteins. In particular, peptides are disclosed which exhibit general binding characteristics to the SH3 domains found in a group of proteins, including but not limited to Abl, Src, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, and p85 PI-3' Kinase. Preferred peptides exhibit selective, if

not specific, binding affinity for the SH3 domain of Src. As described herein, the peptides of the present invention include a core sequence, preferably a consensus sequence, and additional amino acid residues that flank the core sequence.

5 These peptides, including the methods for their identification, are described in greater detail, below.

Thus, in a specific embodiment of the invention, peptides are provided which have at least nine and up to about forty-five amino acid residues, including an amino acid

10 sequence resembling the formula,

R-2-L-P-5-6-P-8-9 (SEQ ID NO:10), positioned anywhere along the peptide. In the above-mentioned formula, each number represents an amino acid residue, such that 2 represents any amino acid residue except

15 cysteine, 5 and 6 each represents a hydrophobic amino acid residue, 8 represents any amino acid residue except cysteine, and 9 represents a hydrophilic amino acid residue except cysteine. Each letter used in the formulas herein represent the standard one-letter symbol for the corresponding amino

20 acid. When the peptide is a 9-mer, the peptide R-P-L-P-P-L-P-T-S (SEQ ID NO:11) is excluded. The peptides of particular interest are those that exhibit a binding affinity for the SH3 domain of Src and Src-related proteins, including Yes, Fyn, Lyn, Lck, Hck and Fgr. Preferably, the

25 peptides of the invention exhibit a binding affinity for the SH3 domain of Src, which is at least three-fold, more preferably at least four-fold, most preferably at least about five-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9). In still other embodiments, the peptides

30 exhibit a binding affinity for the SH3 domain of Src which is at least ten-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9).

In specific embodiments, peptides are disclosed in which the various amino acid residues at the indicated positions

35 may independently have the following preferred identities: 2 is a P, R, A, L, Q, E or S, more preferably P or R; 5 represents a P, M, I or L, more preferably P or M; 6 is a P,

L, I or V, more preferably P or L; 8 is a T, R, P, I, N, E, V, S, A, G or L, more preferably T or R; and 9 is a T, R, S, H or D, more preferably T or R. Despite the preference for hydrophobic amino acid residues at 5 and 6, in some cases it may be desirable to have hydrophilic amino acid residues at these positions. Specifically, amino acid residue 5 may be a T, R or S, and amino acid residue 6 may be a T or R. Likewise, while a hydrophilic amino acid residue is preferred at position 9, in some instances a hydrophobic residue, such as a P or A, may be desirable.

The present invention also contemplates SH3 domain-binding peptides with a minimum length of 10, 11, 12, 13, 14, 15 or more amino acids. Such peptides contain additional amino acid residues flanking the core sequence of R-2-L-P-5-6-P (SEQ ID NO:71) either at the C-terminal end, the N-terminal end or both. Thus, for example, such peptides include those that further comprise a C-terminal-flanking amino acid sequence of the formula 10, 10-11, 10-11-12, 10-11-12-13 (SEQ ID NO:12) or 10-11-12-13-14 (SEQ ID NO:13), in which each number represents any amino acid residue except cysteine, such that the amino acid residue 10 is bound to the amino acid residue 9 by a peptide bond. In that case, specific embodiments include an amino acid residue 10 which is T, R, L, S, D, P, A or N, preferably T or R, an amino acid residue 11 which is R, P, A, Q, S or T, preferably R or P, an amino acid residue 12 which is P, S, R or T, preferably P or S, an amino acid residue 13 which is P, S, R, F, H or T, preferably P or S, and an amino acid residue 14 which is S, R, G or T, preferably S or R.

Furthermore, peptides are also provided which further comprise an N-terminal-flanking amino acid sequence of the formula 1', 2'-1', 3'-2'-1' or 4'-3'-2'-1' (SEQ ID NO:14) in which each number represents any amino acid residue except cysteine, such that 1' is bound to R by a peptide bond. In such a case, specific embodiments are provided in which the amino acid residue 1' is T, P, S, N, F, W, K, H, Q or G, preferably T or P, wherein the amino acid residue 2' is S, T,

G, P, R, Q, L, A or H, preferably S or T, wherein the amino acid residue 3' is R, S, P, G, A, V, Y or L, preferably S or T, and wherein the amino acid residue 4' is R, S, V, T, G, L or F, preferably R or S.

5 In a particular embodiment, a peptide is disclosed having at least thirteen and up to forty-five amino acid residues, including an amino acid sequence of the formula, 3'-2'-1'-R-2-L-P-5-6-P-8-9-10 (SEQ ID NO:15), positioned
10 anywhere along the peptide, in which each number represents an amino acid residue, such that 3', 2', 1', 2, 8, and 10 each represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the
15 corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src. Preferred 13-mers include, but are not limited to, those having an amino acid residue 5 which is a P or M, an amino acid residue 1' which is T, P, S or N, an amino acid residue 2' which is S or T, an
20 amino acid residue 3' which is R or S, and an amino acid residue 10 which is T or R. In all the SH3 domain-binding peptides described herein, the prohibition against the use of the hydrophilic amino acid residue cysteine (C) does not extend beyond the 7-mer "core" sequence and the additional
25 amino acid residues flanking the core up to a total (core + flanking) of about 20 amino acids. That is, the occasional use of a cysteine is not absolutely prohibited. What should be kept in mind is that the potential for the formation of intramolecular disulfide bonds, to form a cyclic structure,
30 be minimized as much as possible. Applicants have found that cyclized structures appear to be disfavored, at least with potential binding peptides of less than about 15 amino acid residues in length. The concern for the formation of cyclized structures comprising the core sequence diminishes
35 with increasing size of the peptide. Presumably, a large enough structure, though cyclic, may allow the critical core sequence to adopt a more or less linear conformation.

In particular, specific peptides are disclosed which exhibit binding affinities to SH3 domains. These include the peptides, RSTPRPLPMLPTTR (SEQ ID NO. 62), RSTPRPLPPLPTTR (SEQ ID NO. 67), GILAPPVPPRNTR (SEQ ID NO. 63), VLKRPLPIPPVTR (SEQ ID NO. 64), GPHRRLPPTPATR (SEQ ID NO. 65), and ANPSPATRPLPTR (SEQ ID NO. 66).

Phage clones are also disclosed, along with the amino acid sequences that are responsible for SH3 domain binding. These phage clones are identified in Figure 5.

10 In other embodiments of the present invention, SH3 domain-binding peptides are contemplated which have a total of 11, 13, 14, 18, 20, 22, 23, 25, 30, 36, 38 or 45 amino acid residues.

The peptides of the present invention, having been disclosed herein, may be prepared by any number of practicable methods, including but not limited to solution-phase synthesis, solid-phase synthesis, protein expression by a transformed host, cleavage from a naturally-derived, synthetic or semi-synthetic polypeptide, or a combination of these techniques.

The SH3 binding peptides exhibit a wide range of biological activity which includes the enhancement (or inhibition, depending on the particular peptide or the nature of the peptide's target molecule, in this case a protein bearing an SH3 domain) of the natural function or biological activity of the peptide's target molecule. For example, the interaction of the binding peptide of the present invention could result in the modulation of the oncogenic activity of the target molecule bearing the SH3 domain. If the target molecule has, in turn, a natural binding partner or ligand, the peptides of the present invention may also exhibit antagonistic or agonistic activity in relation to the biological activity of the natural binding partner.

Thus, it is an object of the present invention to provide a method of activating Src or Src-related protein tyrosine kinases by administering an effective amount of the SH3 domain-binding peptides generally described herein. Th

intensity of the immune response can thus be stimulated, for example, by the increased production of certain lymphokines, such as TNF-alpha and interleukin-1. As is generally known to those of ordinary skill in the art, a more intense immune response may be in order in certain conditions, such as in combating a particularly tenacious infection, viral or otherwise, or a malignancy.

Furthermore, in a specific embodiment of the present invention, a conjugate compound is contemplated which comprises the peptide of the present invention and a second chemical moiety. The second chemical moiety can be selected from a wide variety of chemical compounds including the peptide itself. Typically, however, the second chemical moiety is selected to be other than the peptide of the present invention, including but not limited to an amino acid, a peptide other than an SH3 binding peptide of the present invention, a polypeptide or protein (i.e., the conjugate is a fusion protein), a nucleic acid, a nucleoside, a glycosidic residue (i.e., any sugar or carbohydrate), a label or image-enhancing agent (including metals, isotopes, radioisotopes, chromophores, fluorophores (such as FITC, TRITC, and the like), and enzyme substrates), a drug (including synthetic, semisynthetic, and naturally-occurring compounds), small molecules (e.g., biotin, hormones, factors) and the like.

The peptide of the present invention can be conjugated to the second chemical moiety either directly (e.g., through appropriate functional groups, such as an amine or carboxylic acid group to form, for example, an amine, imine, amide, ester, acyl or other carbon-carbon bond) or indirectly through the intermediacy of a linker group (e.g., an aliphatic or aromatic polyhydroxy, polyamine, polycarboxylic acid, polyolefin or appropriate combinations thereof). Moreover, the term "conjugate," as used herein, is also meant to encompass non-covalent interactions, including but not limited to ionic, affinity or other complexation interactions. Preferably, such other non-covalent

interactions provide definable, most preferably, isolatable chemical conjugate species.

As described further herein, the peptides of the present invention have been shown to localize within certain cellular compartments which contain Src or Src-related proteins. Consequently, the above-described conjugate can be utilized as a delivery system for introduction of a drug to cells, tissues or organs that include SH3 domain-containing proteins.

10 It should also be pointed out that the present invention seeks to provide a recombinant construct comprising a nucleic acid or its complement that includes codons or nucleotide sequences encoding a peptide having a region that binds to an SH3 domain, preferably the Src SH3 domain. The recombinant
15 nucleic acid may be a DNA or RNA polynucleotide.

In a specific embodiment, the present invention contemplates a recombinant construct which is a transforming vector. Such vectors include those well known to those of ordinary skill in the art, which effect the transfer or
20 expression of the nucleotide sequence after introduction to a host, such as recombinant plasmid, phage or yeast artificial chromosome. These vectors may be closed circular loops or they may be linearized. The vectors contemplated include those that exist extrachromosomally after host transformation
25 or transfection, as well as those that integrate within or even displace portions of the host chromosome. The vectors may be introduced to the cell with the help of transfection aids or techniques well-known in the art. For example, these aids or techniques may take the form of electroporation, use
30 of calcium chloride, calcium phosphate, DEAE dextran, liposomes or polar lipid reagents known as LIPOFECTIN or LIPOFECTAMINE. In addition, the present invention contemplates the direct introduction of the desired nucleic acid to the host cell, for instance, by injection.

35 Transformed host cells are also obtained by the methods of the present invention which are capable of reproducing the polynucleotide sequences of interest and/or expressing the

corresponding peptide products. A variety of hosts are contemplated, including prokaryotic and eukaryotic hosts. In particular, bacterial, viral, yeast, animal, and plant cells are potentially transformable hosts. Thus, a method is disclosed to obtain a transformed host cell that can produce, preferably secrete, a peptide having a region that binds to an SH3 domain comprising (a) providing an expression vector, preferably a secretory expression vector, comprising a nucleotide sequence encoding at least one copy of a peptide having a region that binds to an SH3 domain; and (b) introducing the vector to a competent host cell.

The peptides, thus produced, may then be introduced to cells, tissues, organs, or administered to the subject for the purpose of modulating the biochemical activity of the SH3 domain-containing proteins present therein. Accordingly, in specific embodiments of the present invention, compositions are provided which comprise an SH3 domain-binding peptide, including a core sequence and flanking sequences, and a suitable carrier.

The compositions contemplated by the present invention may also include other components, from those that facilitate the introduction or administration of the compositions to those that have their own innate activity, such as a prophylactic, a diagnostic or a therapeutic action. Such innate activity may be distinct from that of the peptides of the present invention or be complementary thereto. In any event, the compositions of the present invention include those that are suitable for administration into mammals, including humans. Preferably, the compositions (including necessarily the carrier) of the present invention are sterile, though others may need only be cosmetically, agriculturally or pharmaceutically acceptable. Still other compositions may be adapted for veterinary use.

The compositions, including the drug delivery systems described herein, are contemplated to be administered in a variety of ways, such as parenterally, orally, intrally, topically or by inhalation. The compositions may also be

administered intranasally, ophthalmically or intravaginally. Furthermore, the compositions of the invention can take several forms, such as solids, gels, liquids, aerosols or patches.

5 In another embodiment of the present invention a method is provided of identifying a peptide having a region that binds to an SH3 domain comprising: (a) providing an immobilized target protein comprising an SH3 domain; (b) incubating the immobilized target protein with an aliquot
10 taken from a phage-displayed random peptide library, which library includes peptides having a random sequence of ≥ 8 amino acid residues; (c) washing unbound phage from the immobilized target protein; (d) recovering the phage bound to the immobilized target protein; and (e) determining the
15 relevant nucleotide sequence of said binding phage nucleic acid and deducing the primary sequence corresponding to the SH3 domain-binding peptide. Preferably, the method further comprises amplifying the titer of the recovered phage and repeating the steps of incubation, washing and recovery to
20 provide SH3 domain-binding peptide-enriched phage.

Any other mode by which the peptide library, random or otherwise, can be "displayed" can be utilized in the present invention, however. Moreover, the present applicants believe that longer random peptide sequences (e.g., >6 amino acid
25 residues, preferably >10 , and most preferably, >12) provide not only much greater diversity but also a richer degree of secondary structure conducive to binding activity. If the random region of the peptide is less than or equal to an 8-mer, it should preferably not be cyclized.

30

5.2. Preparation of Random Peptide Libraries

The preparation and characterization of the preferred phage-displayed random peptide libraries have been described elsewhere. See, for example, Kay, B.K. et al. in
35 Gene (1992) 128:59-65, for a description of the preparation of the phage-displayed random peptide library known as TSAR-9, more below. In particular, by cloning degenerate

oligonucleotides of fixed length into bacteriophag vectors, recombinant librari s of random peptides can be generated which are expressed at the amino-terminus of the pIII protein on the surface of M13 viral particles. (There are 3-5 copies 5 of the pIII-fusion on the surface of each particle.) Phag display offers several conveniences: first, the expressed peptides are on the surface of the viral particles and accessible for interactions; second, the recombinant viral particles are stable (i.e., can be frozen, exposed to pH 10 extremes); third, the viruses can be amplified; and fourth, each viral particle contains the DNA encoding the recombinant genome. Consequently, these libraries can be screened by isolating viral particles that bind to targets. The isolates can be grown up overnight, and the displayed peptide sequence 15 responsible for binding can be deduced by DNA sequencing.

These libraries have approximately $>10^8$ different recombinants, and nucleotide sequencing of the inserts suggests that the expressed peptides are indeed random in amino acid sequence. These libraries are referred to herein 20 as TSAR libraries, where TSAR stands for Totally Synthetic Affinity Reagents. The preparation of the TSAR libraries are described further below.

5.3. SH3 Binding Clones And Their Characteristics

25 Accordingly, peptides have been isolated from an unconstrained random peptide library which exhibit a binding affinity for SH3 domains. Furthermore, the binding affinities exhibited by the disclosed peptides differ in their selectivities with certain peptides showing comparable 30 binding affinities for SH3 domains derived from different proteins, while others manifest greater affinities for specific SH3 domains.

The amino acid sequence of various peptides isolated by the present method are listed in Figure 5. As can be seen 35 from this list, c rtain groups of SH3 domain binding peptides are is lat d from three separat random peptide librari s, each bas d on a different type of random p ptide insert, all

displayed at the amin -terminus of the pIII prot in on the surface of M13 viral particles. T n clon s w re isolated from the R8C library, seven from the TSAR-12 library, and seven from the TSAR-9 library. The sequences are presented 5 to highlight the particular amino acid residues believed to bind directly to the SH3 domain, as well as to point out the remaining amino acid resiudes of the random insert and the viral flanking sequences and complementary site amino acid residues common to each group of clones. The frequency with 10 which each particular clone is found in each library is also indicated in Figure 5. Thus, clones T12.SRC3.1 and T12.SRC3.2 are by far the most abundant clones found among the three libraries.

Interestingly, all the binding peptides are found to 15 have the proline-rich amino acid residue motif, which is apparently responsible for binding, the motif being located predominantly at the C-terminal end of the insert, although each clone also contains an insert at the N-terminal end. The significance of this observation is not presently 20 understood, although this finding may indicate the possible importance of the C-terminal viral flanking sequences in SH3 domain binding.

Indeed, a synthetic peptide bearing only the core consensus sequence RPLPPLP (SEQ ID NO:9) was less effective 25 in binding to target SH3 domains than synthetic peptides that also included additional amino acid residues flanking the core sequences. Thus, 13-mers and 14-mers having the sequences RSTPRPLPMLPTTR (SEQ ID NO:62), RSTPRPLPPLPTTR (SEQ ID NO:67), GILAPPVPPRNTR (SEQ ID NO:63), GPHRRLPPTPATR (SEQ 30 ID NO:65), and VLKRPLPIPPVTR (SEQ ID NO:64) have been prepared and shown to bind to SH3 domains, such as those of Src and Yes, much more avidly than the 7-mer, RPLPPLP (SEQ ID NO:9). The 13-mer ANPSPATRPLPTR (SEQ ID NO:66) has been shown to have binding affinities comparable to the core 35 consensus sequenc . In each case, the 13-mers comprise a 7-mer "core" sequence plus additional amino acid residues

flanking same, some of which additional amino acid residues are contributed by the viral flanking sequences.

Thus, in one embodiment of the present invention, a 7-mer core includes a consensus motif of the formula RXLP $\phi\phi$ P
 5 (SEQ ID NO:71), wherein R is arginine, L is leucine, P is proline, X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue. By "hydrophobic amino acid residue," the applicants mean to include F, Y, W, V, A, I, L, P or M, each letter representing the standard
 10 one-letter designation for the corresponding amino acid residue.

Furthermore, a preferred 9-mer peptide comprising two additional amino acids on the C-terminal end of the core sequence is envisioned having a consensus motif of the
 15 formula RXLP $\phi\phi$ PX ψ . In this preferred 9-mer consensus motif, the symbol ψ represents a hydrophilic amino acid residue, except cysteine. By "hydrophilic amino acid residue," the applicants mean to include K, R, H, D, E, N, Q, T, S or C, and the other symbols are as defined above. For the purposes
 20 of the present invention, a glycine residue (G) may be considered either a hydrophobic or a hydrophilic amino acid residue. The one-letter symbols B and Z, which stand for N or D and Q or E, respectively, are considered hydrophilic amino acid residues.

25 Particular 13-mer peptides of the present invention include those listed, below. It is noted, however, that not all the following 13-mer peptides correlate strictly to or comply with the preferred 9-mer consensus motif, described above. Those peptides that do not comply (indicated in
 30 italics, with the non-complying amino acid residues underscored) can, thus, be described as "resembling" those that do comply (indicated in normal type) with the preferred 9-mer consensus motif: PGFRELPLPPSR (SEQ ID NO:72), AQSRLPIPPETR (SEQ ID NO:73), VLKRPLPIPPVTR (SEQ ID NO:64),
 35 PPNSPLPLPTHL (SEQ ID NO:74), TGRGPLPLPNDS (SEQ ID NO:75), YSTRPVPPITRPS (SEQ ID NO:76), SHKSRLLPLPTRP (SEQ ID NO:77), YRFRALPSPPSAS (SEQ ID NO:78), GPHRRLPPTPATR (SEQ ID NO:65),

LAQRQLPPTPGRD (SEQ ID NO:79), ALQRRLPRTPPPA (SEQ ID NO:80),
 PATRPLPTRPSRT (SEQ ID NO:81), YSTRPLPSRPSRT (SEQ ID NO:82),
 XPGRILLPSEPR (SEQ ID NO:83), SGGILAPPVPPRN (SEQ ID NO:84),
 RSTRPLPILPRTT (SEQ ID NO:85), STPRPLPMLPTTR (SEQ ID NO:86),
 5 STNRPLPMIPTTR (SEQ ID NO:87), RSTRPLPSLPITT (SEQ ID NO:88),
 STSRPLPSLPITT (SEQ ID NO:89), RSTRSLPPLPPTT (SEQ ID NO:90),
 RSTRQLPIPPTTT (SEQ ID NO:91), STPRPLPLIPTTP (SEQ ID NO:92),
 RSTRPLPPTPLTT (SEQ ID NO:93), and RSTRPQPPPPITT (SEQ ID
 NO:94). Accordingly, other peptides not specifically
 10 disclosed, which either comply with or "resemble" the
 preferred 9-mer consensus motif, can be readily envisioned by
 those of ordinary skill in the art and are considered to be
 equivalent to those that are specifically disclosed above.
 In particular, non-compliance at positions 1 (S, G, and I, in
 15 place of R, are tolerated), 3 (V, A, and Q, in place of L,
 are tolerated), 4 (L, in place of P, is tolerated), 5
 (hydrophilic amino acid residues, S, R, and T, are tolerated,
 in place of a hydrophobic amino acid residue), 6 (hydrophilic
 amino acid residues, R and T, are tolerated in place of a
 20 hydrophobic amino acid residue), 7 (T, and S, in place of P,
 are tolerated), and 9 (P and A are tolerated in place of a
 hydrophilic amino acid residue) have been observed.

5.3.1. Binding Specificities

25 It has been discovered that certain of the
 binding peptides disclosed have a greater relative binding
 affinity for one SH3 domain over another. Referring now to
 Figure 8, the relative binding affinities of the various
 peptides described above toward different SH3 domain targets
 30 are graphically presented. As one can see, the relative
 binding affinities of the respective peptides can differ by
 orders of magnitude. Thus, as shown in Figure 8, the peptide
 GPHRRLPPTPATR (SEQ ID NO:65), having the relevant sequence of
 the phage clone identified as T12.SRC3.3, is specific to Src
 35 family SH3 domains, including, but not limited to, Src, Yes,
 Lck, Hck, Fgr, Fyn, and Lyn. This SH3 binding peptide has
 little affinity for SH3 domains derived from PLC γ or Grb2.

On the other hand, the peptide GILAPPVPPRNTR (SEQ ID NO:63), corresponding to the relevant sequence of the phage clone T12.SRC3.1, which is one of the most abundant binding clones found by the present method, binds generically to a broad range of SH3 domains, including Src, PLC γ , and Grb2.

On an intermediate level, the present invention has also uncovered a peptide, VLKRPLPIPPVTR (SEQ ID NO:64), corresponding to the relevant sequence of the phage clone T12.SRC3.6, which is Src preferential; that is, this peptide exhibits strong binding affinities for members of the Src family, some binding affinities for Grb2 proteins, but little binding affinities for PLC γ domains. The peptide ANPSPATRPLPTR (SEQ ID NO:66), corresponding to the relevant sequence of the phage clone T12.SRC3.2, also exhibits Src family specificity similar to GPHRRLPPTPATR (SEQ ID NO:65). The peptides RSTPRPLMLPTTR (R8C.YES3.5; SEQ ID NO:62) and RSTPRPLPLPTTR (representative consensus motif; SEQ ID NO:67) are highly specific for SH3 domain of Src, Yes, and other Src-related proteins.

20

5.4. Further Discussion of Binding Experiments

At the outset it is apparent that the binding affinity of certain peptides to the SH3 domain of Src and Src-related proteins is governed by more than just the presence of the preferred core consensus sequences, RPLPPLP (SEQ ID NO:9) or RPLMLP (SEQ ID NO:95; i.e., RPLP(P/M)LP, SEQ ID NO:96). Thus, while the synthetic peptides RSTPRPLMLPTTR (R8C.YES3.5; SEQ ID NO:62) and RSTPRPLPLPTTR (consensus; SEQ ID NO:67) exhibit a strong specific binding affinity for Src SH3, the other synthetic peptides tested also exhibited an avid binding affinity to SH3 domains relative to the 7-mer, RPLPPLP (SEQ ID NO:9). These other peptides, GILAPPVPPRNTR (SEQ ID NO:63), VLKRPLPIPPVTR (SEQ ID NO:64), GPHRRLPPTPATR (SEQ ID NO:65), and ANPSPATRPLPTR (SEQ ID NO:66), sport core sequences and flanking sequences that do not closely adhere to the preferred core consensus sequences. Thus, these results suggest that binding affinity

to SH3 domains is governed to a large extent by the nature of the amino acid residues flanking the core 7-mer sequence.

The binding characteristics of Src SH3-selected peptides was determined using synthetic biotinylated peptides

5 corresponding to the sequences displayed by Src SH3-selected phage. These biotinylated peptides were assayed for direct binding to immobilized Src SH3-GST. Each of the five library-derived peptides tested were found to bind to Src SH3-GST and Yes SH3-GST over background (Figure 8).

10 Furthermore, a strong correlation was observed between the similarity of a given peptide to the preferred core consensus sequence RPLP(P/M)LP and the peptide's affinity for Src SH3-GST. The core sequence of the clone T12.SRC3.1

(GILAPPVPPRNTR; SEQ ID NO:63) appears to provide more generic

15 SH3 domain-binding characteristics.

Experiments comparing the relative binding of various phage clones to SH3 domains taken from a variety of proteins demonstrated the preference of these clones for Src and Src-related SH3 domains over SH3 domains taken from other

20 proteins.

It was further found that while the 7-mer having the consensus sequence RPLPPLP (SEQ ID NO:9) bound to Src SH3-GST only weakly, peptides comprising the consensus sequence flanked by residues encoded by one of the Src SH3-selected

25 clones (R8C.YES3.5), RSTP (SEQ ID NO:97) at the N-terminal end and TTR at the C-terminal end, bound significantly better than any of the peptides tested (Figure 7). Thus, as stated previously, sequences that flank the RPLP(P/M)LP (SEQ ID NO:96) core appear to be important contributors to SH3

30 binding. It is further surmised that a peptide having or resembling the sequence RSTPAPPVPPRTTR (SEQ ID NO:98) should exhibit strong but generic binding to a variety of SH3 domains.

Similarly, it is observed that most of the Src SH3-
35 binding motifs are located near the carboxy-terminus of the random peptides, adjacent to sequences which are fixed in every clone (Figure 5). The exceptional clones tend to

poss ss sequenc s that resemble motifs that include fixed flanking s quences. This clustering contrasts with previ us results, in which binding motifs are distributed throughout the random peptide. Kay, B.K., et al., in Gene (1993)

5 128:59-65.

The binding of the library-derived Src SH3-binding peptides was compared to that of peptides corresponding to proline-rich regions of natural proteins. Peptides corresponding to SH3-binding regions in human PI-3' Kinase
10 (KISPPTPKPRPPRPLPV; SEQ ID NO:69) and human SOS1.20 (GTVEPVPPPVPPIRRRPESA; SEQ ID NO:68), as well as a proline-rich region of the cytoskeletal protein vinculin (LAPPKPPLPEGEV; SEQ ID NO:70), bound Src SH3 less well than the library-derived peptides (Figure 7).

15 As mentioned above, the relative specificity of binding was explored. Thus, the relative binding of Src SH3-select d peptides to equal amounts of GST fusions to SH3 domains from different proteins was determined (Figure 8). While all of the library-derived peptides bound the Src and Yes SH3
20 domains almost equally well, none of the peptides (with the exception of peptide T12.SRC3.1, the most divergent peptide tested) bound the SH3 domains of Grb2, Crk, Abl or PLC γ 1 appreciably. Thus, the library-derived peptides, in contrast with a peptide derived from SOS1, exhibit SH3 binding that is
25 relatively specific for Src-family members.

Next, it was determined whether the binding to the Src SH3 domain was qualitatively like the interactions of the SH3 domain and natural proteins found in cell lysates. Thus, radiolabeled proteins were prepared from NIH 3T3 cell lysates
30 and chromatographed over Src SH3-GST immobilized on glutathione linked Sepharose. SDS-PAGE shows that a number of proteins can be affinity purified in this manner. The synthesized peptides bind quite well to the Src SH3 domain, as they can compete the binding of radiolabeled proteins from
35 cell lysates to immobiliz d Src-GST, with an IC $_{50}$ of 1-10 mM (Figure 9). In conclusion, the peptides can efficiently

block the interaction of cellular proteins with Src SH3 in vitro.

Moreover, *Xenopus laevis* oocytes injected with mRNA encoding constitutively active Src undergo progesterone-
5 induced maturation at an accelerated rate relative to oocytes injected with water or c-Src mRNA. Unger, T.F. and Steele, R.E. in Mol. Cell.Biol. (1992) 12:5485-5498. To explore the ability of the library-derived Src SH3-binding peptides to exert a biochemical effect in vivo, the influence of the
10 peptides on the maturation of *Xenopus laevis* oocytes was examined. Hence, stage VI oocytes were injected with peptide, exposed to progesterone, and scored for germinal vesicle breakdown. Figure 10 shows that the rate of maturation was accelerated by approximately one hour when
15 oocytes were injected with the SH3-binding peptide consisting of RPLPPLP (SEQ ID NO:9) flanked by residues from clone T12.SRC3.6 (VLKRPLPIPPVTR; SEQ ID NO:64), but not with water or a peptide corresponding to a proline-rich segment of vinculin (LAPPKPPLPEGEV; SEQ ID NO:70) as controls. The
20 magnitude of this effect is roughly equivalent to that seen with injection of mRNA encoding constitutively active Src. See, e.g., Figure 3B in Unger, T.F. and Steele, R.E., *supra*. This result suggests that the library-derived Src SH3-binding peptide is effectively relieving an inhibitory effect of the
25 Src SH3 domain upon Src PTK activity. This model is consistent with a number of studies which have demonstrated an inhibitory effect of the Src SH3 domain upon Src kinase and transforming activity. See, e.g., Okada, M., et al., *supra*; Murphy, S.M., et al., *supra*; and Superti-Furga, G., et
30 al., *supra*.

5.5. Diagnostic And Therapeutic Agents Based On SH3 Binding Peptides and Additional Methods of Their Use

As already indicated above, the present invention
35 also seeks to provide diagnostic, prophylactic, and

therapeutic agents based on the SH3 binding peptides described herein.

In one embodiment, diagnostic agents are provided, preferably in the form of kits, comprising an SH3 domain-
5 binding peptide and a detectable label conjugated to said peptide directly, indirectly or by complexation, said peptide comprising: (i) a core sequence motif of the formula RXLP ϕ ϕ P (SEQ ID NO:71), wherein X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue,
10 including F, Y, W, V, A, I, L, P, M or G, each letter representing the standard one-letter designation for the corresponding amino acid residue; and (ii) two or more additional amino acid residues flanking said core sequence at its C-terminal end, N-terminal end or both.

15 The diagnostic agents of the present invention can be used to detect the presence of SH3 domains of a generic or specific type in cells, tissues or organs either *in vitro* or *in vivo*. For *in vivo* applications, the diagnostic agent is preferably mixed with a pharmaceutically acceptable carrier
20 for administration, either enterally, parenterally or by some other route dictated by the needs of the particular application.

In a particular embodiment, for example, an assay based on a fusion product is contemplated which comprises a Src SH3
25 domain-binding peptide of the invention and a substrate for deregulated or "activated" Src. For instance, a muscle biopsy, taken from a subject suspected of being infected by the Rous sarcoma virus, can be treated with an effective amount of the fusion product. By subsequent analysis of the
30 degree of conversion of the substrate, one can potentially detect infection by the Rous sarcoma virus in the subject, particularly mammals, especially chickens. The presence of the retrovirus, which causes the expression of deregulated or "activated" Src, may thus be indicated by unusually high
35 levels of Src as revealed by large amounts of the converted substrate. See, for example, Paxton, W.G. et al., in Biochem. Biophys. Res. Commun. (1994) 200(1):260-267

(d tection of phosphorylated tyrosine and serine residu s of angiotensin II AT1 r ceptor, a ubstrate of Src family tyrosine kinases); another suitable substrate may be th protein p68 (Fumagalli, S. et al., in Nature (1994)

5 368(6474):871-874; Taylor, S.J. and Shalloway, D., in Ibid. at 867-871.

Alternatively, the enzyme can be isolated by selective binding to a form of the SH3 domain-binding peptides of the present invention (e.g., biotin-peptide conjugate). After
10 isolation of the protein-peptide conjugate complex (e.g., on a column comprising streptavidin), the activity of the enzyme can then be assayed by conventional methods to determine its level of protein kinase activity which can be taken as an indication of the presence of the deregulated or "activated"
15 form of the enzyme. An assay for Src kinase has been described by Klinz and Maness, in Neuroprotocols (a companion to Neuroscience) (1992) 1(3):224-231.

Moreover, the diagnostic agents of the invention can also serve as imaging agents of cells, tissues or organs,
20 especially those that contain proteins with an SH3 domain. For example, neural cells (e.g., neurons, other areas of the brain), osteoclasts, osteoblasts, platelets, immune cells, and other dividing cells are known to express or contain proteins with SH3 domains. Thus, an image can be taken of
25 portions of the body to serve as a baseline for subsequent images to detect physiologic or biochemical changes in the subject's body. For instance, changes in the condition of cellular levels of Src or a transformation of the cellular Src to an "activated" form may be detected using the
30 diagnostic or imaging agents of the present invention.

Accordingly, it has been demonstrated that an SH3-binding peptide tagged with a fluorescence emitter can provide an image of the cytoskeleton. The images are presented in Figure 11. As can be seen from Figure 11,
35 pan ls A, B, and C show the fluorescence image that is obtain d on treating NIH 3T3 fibroblasts with SH3 domain-binding peptides modified to include a fluorescent tag. In

sharp contrast, panel D shows only a dark image that is produced when the cells are treated with a proline-rich segment of vinculin as a control.

In another embodiment, an SH3 domain-binding peptide-
5 horseradish immunoperoxidase complex or related immunohistochemical agent could be used to detect and quantitate specific receptor molecules in tissues, serum or body fluids. In particular, the present invention provides useful diagnostic reagents for use in immunoassays, Southern
10 or Northern hybridization, and *in situ* assays. Accordingly, the diagnostic agents described herein may be suitable for use *in vitro* or *in vivo*.

In addition, the diagnostic or imaging agent of the present invention is not limited by the nature of the
15 detectable label. Hence, the diagnostic agent may contain one or more such labels including, but not limited to, radioisotope, fluorescent tags, paramagnetic substances, heavy metals, or other image-enhancing agents. Those of ordinary skill in the art would be familiar with the range of
20 label and methods to incorporate or conjugate them into the SH3 domain-binding peptide to form diagnostic agents.

In yet a further embodiment, pharmaceutical compositions are provided comprising an SH3 domain-binding peptide and a pharmaceutically acceptable carrier. In a specific
25 embodiment of the invention, the pharmaceutical composition is useful for the modulation of the activity of SH3 domain-containing proteins. By "modulation" is meant either inhibition or enhancement of the activity of the protein target. Accordingly, a pharmaceutical composition is
30 disclosed comprising an SH3 domain-binding peptide and a pharmaceutically acceptable carrier, said peptide comprising:
(i) a 9-mer sequence motif of the formula RXLP ϕ PX ψ (SEQ ID NO:10), wherein X represents any amino acid except cysteine, ϕ represents a hydrophobic amino acid residue, and wherein ψ
35 is a hydrophilic amino acid residue except cysteine, each letter representing the standard one-letter designation for the corresponding amino acid residue; and, optionally, (ii)

additional amino acid residues flanking the 9-mer sequence at its C-terminal end, N-terminal end or both, up to a total of 45 amino acid residues, including said 9-mer sequence.

Preferably, the peptide comprises at least one, more preferably at least two, and most preferably at least three additional amino acids flanking the 9-mer sequence.

As stated above, the therapeutic or diagnostic agents of the invention may also contain appropriate pharmaceutically acceptable carriers, diluents and adjuvants. Such

10 pharmaceutical carriers can be sterile liquids, such as water and oils including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered

15 intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel,

20 magnesium carbonate, magnesium stearate, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. These compositions can take the form of solutions, suspensions, tablets, pills, capsules, powders, sustained-

25 release formulations and the like. Suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin.

Such compositions will contain an effective therapeutic amount of the active compound together with a suitable amount

30 of carrier so as to provide the form for proper administration to the subject. While intravenous injection is a very effective form of administration, other modes can be employed, including but not limited to intramuscular, intraperitoneal, and subcutaneous injection, and oral, nasal,

35 enteral, and parenteral administration.

The therapeutic agents and diagnostic agents of the invention are used for the treatment and/or diagnosis

of animals, and more preferably, mammals including humans, as well as dogs, cats, horses, cows, pigs, guinea pigs, mice and rats. Accordingly, other methods contemplated in the present invention, include, but are not limited to, a method of
5 modulating, i.e., inhibiting or enhancing, bone resorption in a mammal (see, e.g., Hall, T.J., in Biochem. Biophys. Res. Commun. (1994) 199(3):1237-44), a method of disrupting protein tyrosine kinase-mediated signal transduction pathways or a method of regulating the processing, trafficking or
10 translation of RNA in a cell by introducing or administering an effective amount of an SH3 domain-binding peptide of the present invention (see, e.g., Taylor, S.J. and Shalloway, D., *supra*).

The diagnostic or therapeutic agents of the present
15 invention can be modified by attachment to soluble macromolecules such as proteins, polysaccharides, or synthetic polymers. For example, the peptide could be coupled to styrene-maleic acid copolymers (see, e.g., Matsumura and Maeda, Cancer Res. (1986) 46:6387),
20 methacrylamide copolymers (Kopeček and Duncan, J. Controlled Release (1987) 6:315), or polyethylene glycol (PEG) (e.g., Hershfield and Buckley, N. Engl. J. Med. (1987) 316:589; Ho et al., Drug Metab. Dispos. (1986) 14:349; Chua et al., Ann. Intern. Med. (1988) 109:114). The agents, if desired,
25 are further targeted by attachment to an antibody, especially a monoclonal antibody. Such antibodies include but are not limited to chimeric, single chain, Fab fragments, and Fab expression libraries. In one embodiment the agent is coupled to the macromolecule via a degradable linkage so that it will
30 be released in vivo in its active form.

In another embodiment, the therapeutic or diagnostic agent may be delivered in a vesicle, in particular a liposome. See, Langer, Science (1990) 249:1527-1533; Treat et al., in Liposomes in the Therapy of Infectious Disease
35 and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York (1989) pp. 353-365; Lopez-Berestein, *ibid.*, pp. 317-327.

In yet another embodiment, the therapeutic or *in vivo* diagnostic agent can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, CRC Crit. Ref. Biomed. Eng. (1987) 14:201; 5 Buchwald et al., Surgery (1980) 88:507; Saudek et al., N. Engl. J. Med. (1989) 321:574). In another embodiment, polymeric materials may be used (see Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida, 1974; Controlled Drug Bioavailability, Drug 10 Product Design and Performance, Smolen and Ball (eds.) Wiley, New York 1984; Raner and Peppas, J. Macromol. Sci. Rev. Macromol. Chem. (1983) 23:61; see, also, Levy et al., Science (1985) 228:190; During et al., Ann. Neurol. (1989) 25:351; Howard et al., J. Neurosurg. (1989) 71:105). In a preferred 15 embodiment, a controlled release system may be placed next to the therapeutic target, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in Medical Applications of Controlled Release, *supra*, (1984) 2:115-138). It will be recognized by one of ordinary skill in the art that a 20 particular advantage of the invention is that a peptide will not be subject to the problems of denaturation and aggregation associated with proteins held in the warm, moist environment of a body in a controlled release system.

Other controlled release systems are discussed in the 25 review by Langer, in Science (1990) 249:1527-1533.

30

35

6. EXAMPLES

6.1. Preparation of the TSAR-9 Library

6.1.1. Synthesis and Assembly of Oligonucleotides

Figure 1 shows the formula of the oligonucleotides and the assembly scheme used in construction of the TSAR-9 library. The oligonucleotides were synthesized with an applied Biosystems 380a synthesizer (Foster City, CA), and the full-length oligonucleotides were purified by HPLC.

Five micrograms of each of the pair of oligonucleotides were mixed together in buffer (10 mM Tris-HCl, pH 8.3, 15 mM KCl, 0.001% gelatin, 1.5 mM magnesium chloride), with 0.1 % Triton X-100, 2 mM dNTP's, and 20 units of Taq DNA polymerase. The assembly reaction mixtures were incubated at 72 °C for 30 seconds and then 30 °C for 30 seconds; this cycle was repeated 60 times. It should be noted that the assembly reaction is not PCR, since a denaturation step was not used. Fill-in reactions were carried out in a thermal cycling device (Ericomp, LaJolla, CA) with the following protocol: 30 seconds at 72 °C, 30 seconds at 30 °C, repeated for 60 cycles. The lower temperature allows for annealing of the six base complementary region between the two sets of the oligonucleotide pairs. The reaction products were phenol/chloroform extracted and ethanol precipitated. Greater than 90% of the nucleotides were found to have been converted to double stranded synthetic oligonucleotides.

After resuspension in 300 µL of buffer containing 10 mM Tris-HCl, pH 7.5, 1 mM EDTA (TE buffer), the ends of the oligonucleotide fragments were cleaved with Xba I and Xho I (New England BioLabs, Beverly, MA) according to the supplier's recommendations. The fragments were purified by 4% agarose gel electrophoresis. The band of correct size was removed and electroeluted, concentrated by ethanol precipitation and resuspended in 100 µL TE buffer. Approximately 5% of the assembled oligonucleotides can be expected to have internal Xho I or Xba I sites; however, only

the full-length molecules were used in the ligation step of the assembly scheme. The concentration of the synthetic oligonucleotide fragments was estimated by comparing the intensity on an ethidium bromide stained gel run along with 5 appropriate quantitated markers. All DNA manipulations not described in detail were performed according to Maniatis, *supra*.

To demonstrate that the assembled enzyme digested oligonucleotides could be ligated, the synthesized DNA 10 fragments were examined for their ability to self-ligate. The digested fragments were incubated overnight at 18 °C in ligation buffer with T4 DNA ligase. When the ligation products were examined by agarose gel electrophoresis, a concatamer of bands was visible upon ethidium bromide 15 staining. As many as five different unit length concatamer bands (i.e., dimer, trimer, tetramer, pentamer, hexamer) were evident, suggesting that the synthesized DNA fragments were efficient substrates for ligation.

20 6.1.2. Construction of Vectors

The construction of the M13 derived phage vectors useful for expressing a TSAR library has been recently described (Fowlkes, D. et al. BioTech. (1992) 13:422-427). To express the TSAR-9 library, an M13 derived 25 vector, m663, was constructed as described in Fowlkes. The m663 vector contains the pIII gene having a *c-myc*-epitope, i.e., as a stuffer fragment, introduced at the mature N-terminal end, flanked by *Xho* I and *Xba* I restriction sites (see also, Figure I of Fowlkes).

30

6.1.3. Expression of the TSAR-9 Library

The synthesized oligonucleotides were then ligated to *Xho* I and *Xba* I double-digested m663 RF DNA containing, the pIII gene (Fowlkes) by incubation with ligase 35 overnight at 12 °C. More particularly, 50 ng of vector DNA and 5 ng of the digested synthesized DNA and was mixed together in 50 µL ligation buffer (50 mM Tris, pH 8.0, 10 mM

MgCl₂, 20 mM DTT, 0.1 mM ATP) with T4 DNA ligase. After overnight ligation at 12°C, the DNA was concentrated by thanol precipitation and washed with 70% thanol. The ligated DNA was then introduced into *E. coli* (DH5αF'; GIBCO 5 BRL, Gaithersburg, MD) by electroporation.

A small aliquot of the electroporated cells was plated and the number of plaques counted to determine that 10⁸ recombinants were generated. The library of *E. coli* cells containing recombinant vectors was plated at a high density 10 (~400,000 per 150 mm petri plate) for a single amplification of the recombinant phage. After 8 hr, the recombinant bacteriophage were recovered by washing each plate for 18 hr with SMG buffer (100 mM NaCl, 10 mM Tris-HCl, pH 7.5, 10 mM MgCl₂, 0.05% gelatin) and after the addition of glycerol to 15 50% were frozen at -80 °C. The TSAR-9 library thus formed had a working titer of ~2 x 10¹¹ pfu/ml.

6.2. Preparation of TSAR-12 Library

Figure 2 shows the formula for the synthetic 20 oligonucleotides and the assembly scheme used in the construction of the TSAR-12 library. As shown in Figure 2, the TSAR-12 library was prepared substantially the same as the TSAR-9 library described in Section 6.1 above with the following exceptions: (1) each of the variant non-predicted 25 oligonucleotide sequences, i.e., NNB, was 30 nucleotides in length, rather than 54 nucleotides; (2) the restriction sites included at the 5' termini of the variant, non-predicted sequences were Sal I and Spe I, rather than Xho I and Xba I; and (3) the invariant sequence at the 3' termini to aid 30 annealing of the two strands was GCGGTG and CGCCAC rather than CCAGGT and GGTCCA (5' to 3').

After synthesis including numerous rounds of annealing and chain extension in the presence of dNTP's and Tag DNA polymerase, and purification as described above in Section 35 6.1.1, the synthetic double stranded, oligonucleotide fragments were digested with Sal I and Spe I restriction enzymes and ligated with T4 DNA ligase to the nucleotide

sequence encoding the M13 pIII gene contained in the m663 vector to yield a library of TSAR-expression vectors as described in Sections 6.1.2 and 6.1.3. The ligated DNA was then introduced into *E. coli* (DH5 α F'; GIBCO BRL, Gaithersburg, MD by electroporation. The library of *E. coli* cells were plated at high density (~400,000 per 150 mm petri plate) for amplification of the recombinant phage. After about 8 hr, the recombinant bacteriophage were recovered by washing, for 18 hr with SMG buffer and after the addition of glycerol to 50% were frozen at -80 °C.

The TSAR-12 library thus formed had a working titer of $\sim 2 \times 10^{11}$ pfu/mL.

6.3. Characterization of the TSAR-9 and -12 Libraries

The inserted synthetic oligonucleotides for each of the TSAR libraries, described in Sections 6.1 and 6.2 above, had a potential coding complexity of 20^{36} ($\sim 10^{47}$) and 20^{20} , respectively, and since $\sim 10^{14}$ molecules were used in each transformation experiment, each member of these TSAR libraries should be unique. After plate amplification the library solution or stock has 10^4 copies of each member/mL.

It was observed that very few (<10%) of the inserted oligonucleotide sequences characterized so far in both of the libraries have exhibited deletions or insertions. This is likely a reflection of the accuracy assembling the oligonucleotides under the conditions used and the fact that certain types of mutations (i.e., frame-shifts) would not be tolerated as pIII an essential protein for phage propagation.

In order to determine whether any coding bias existed in the variant non-predicted peptides expressed by these libraries, perhaps due to biases imposed in vitro during synthesis of the oligonucleotides or in vivo during expression by the reproducing phage, inserts were sequenced as set forth below.

6.3.1. Characterization of TSAR-9 Library

Insert d synthetic oligonucleotide fragments of 23 randomly chosen isolates were examined from the TSAR-9 library. Individual plaques were used to inoculate 1 ml of 2XYT broth containing *E. coli* (DH5 α F') cells and the cultures were allowed to grow overnight at 37°C with aeration. DNA was isolated from the culture supernatants according to Maniatis, *supra*. Twenty-three individual isolates were sequenced according to the method of Sanger (Proc. Natl. Acad. Sci. USA (1979) 74:5463-5467) using as a primer the oligonucleotide 5'-AGCGTAACGATCTCCCG (SEQ ID NO. 99), which is 89 nucleotides downstream of the pIII gene cloning site of the m663 vector used to express the TSARS.

Nucleotide sequences and their encoded amino acid sequences were analyzed with the MacVector computer program (IBI, New Haven, CT). The Microsoft EXCEL program was used to evaluate amino acid frequencies. Such analyses showed that the nucleotide codons coding for and hence most amino acids, occurred at the expected frequency in the TSAR-9 library of expressed proteins. The notable exceptions were glutamine and tryptophan, which were over- and under-represented, respectively.

It is of interest to note the paucity of TAG stop codons in the inserts, i.e., only 2 of ~200 isolates characterized contained a TAG stop codon. About half [1-(47/48)³⁶] of the phage inserts were expected to have at least one TAG codon in view of the assembly scheme used. However, most of the TAG-bearing phage appear to have been lost from the library, even though the bacterial host was *supE*. This may be a consequence of suppression being less than 100% effective.

The amino acids encoded by the inserted double strand d synthesized oligonucleotide sequences, excluding the fixed PG-encoding centers, were concatenated into a single sequence and the usage frequency determined for each amino acid using the Microsoft EXCEL program. These frequencies were compared to that expected from the assembly scheme of the oligonucleotides, and the divergence from expected values represented by the size of the bars above and below the

baseline. Chi square analysis was used to determine the significance of the deviations. The majority of amino acids were found to occur at the expected frequency, with the notable exceptions that glutamine and tryptophan were somewhat over- and under-represented, respectively. Thus, except for the invariant Pro-Gly, any position could have any amino acid; hence, the sequences are unpredicted or random.

6.3.2. Characterization of TSAR-12 Library

Approximately 10 randomly chosen inserted oligonucleotides from the TSAR-12 library were examined by DNA sequencing as described above in Section 6.3.1. The isolates were chosen at random from the TSAR-12 library and prepared for sequencing, as were the TSAR-9 isolates. Analysis showed that except for the invariant Gly any position could have any amino acid; hence, the sequences are unpredicted or random.

6.4. Preparation of RSC Library

Referring now to Figure 3, two oligonucleotides were synthesized on an Applied Biosystems Model 380a machine with the sequence 5'-TGACGTCTCGAGTTGTNNKNNKNNKNNKNNKNNKNNKNNKTGTGGATCTAGAAGGATC-3' (SEQ ID NO:31) and 5'-GATCCTTCTAGATCC-3' (SEQ ID NO:32), where N is an equimolar ratio of deoxynucleotides A, C, G, and T, and K is an equimolar ratio of G and T. Fifty pmol of each oligonucleotide was incubated at 42 °C for 5 min, then 37 °C for 15 min, in 50 µL of Sequenase™ buffer (U.S. Biochemicals, Cleveland, OH) with 0.1 µg/µL acetylated BSA, and 10 mM DTT. After annealing, 10 units of Sequenase™ (U.S. Biochemicals) and 0.2 mM of each dNTP were added and incubated at 37 °C for 15 min. The sample was then heated at 65 °C for 2 hr, digested with 100 units of both Xho I and Xba I (New England BioLabs, Beverly, MA), phenol extracted, ethanol precipitated, and resolved on a 15% non-denaturing polyacrylamide gel. The assembled, digested fragment was gel purified prior to ligation. The vector, m663 (Fowlkes, D. t

al. Biotech. (1992) 13:422-427), was prepared by digestion with *Xho* I and *Xba* I, calf alkaline phosphatase (Boehringer Mannheim, Indianapolis, IN) treatment, phenol extracted, and purified by agarose gel electrophoresis. To ligate, 20 µg vector was combined with 0.2 µg insert in 3 mL with T4 DNA ligase (Boehringer Mannheim), according to the manufacturer. After removal of the protein and buffer by phenol extraction and ethanol precipitation, the ligated DNA was electroporated into XL1-Blue *E. coli* (Stratagene, San Diego, CA) and plated for eight hours at 37 °C. To recover the recombinant phage, the top agar was collected with a spatula, mixed with an equal volume of 100 mM NaCl, 10 mM MgCl₂, and 50 mM Tris-HCl (pH7.5), and disrupted by two passes through an 18-gauge syringe needle. The bacterial cells were removed by centrifugation, and phage particles were collected by polyethylene glycol precipitation and stored at -70 °C in 25% glycerol. The library had 10⁸ total recombinants and a working titer of 6 x 10¹³ pfu/mL.

Members of the library were checked for inserts by the polymerase chain reaction (Saiki, et al. Science (1988) 239:487-491). Individual plaques on a petri plate were touched with a sterile toothpick and the tip was stirred into 2xYT with F⁺*E. coli* bacteria and incubated overnight at 37 °C with aeration. Five microliters of the phage supernatant were then transferred to new tubes containing buffer (67 mM Tris-HCl, pH 8.8/10 mM β-mercaptoethanol/16.6 mM ammonium sulfate/6.7 mM EDTA/50 µg bovine serum albumin per mL), 0.1 mM deoxynucleotide triphosphates, and 1.25 units of *Taq* DNA polymerase (Boehringer Mannheim, Indianapolis, IN) with 100 pmoles of oligonucleotide primers. The primers flanked the cloning site in gene III of m663 (5'-TTCACCTCGAAAGCAAGCTG-3' (SEQ ID NO:100) and 5'-CCTCATAGTTAGCGTAACG-3' (SEQ ID NO:101)). The assembly reactions were incubated at 94 °C for 1 min, 56 °C for 2 min, and 72 °C for 3 min; this cycle was repeated 24 times. The reaction products were then resolved by electrophoresis on a NuSieve 2.0% agarose gel (FMC, Rockland, ME). Gels revealed

that for 20 plaques tested, all were recombinant and had single inserts of the expected size.

Based on the sample size of the library, it was anticipated that 100% of the recombinants had single inserts. However, all of the SH3-binding phage isolated from the R8C library had double-inserts. Such phage are presumed rare (i.e., <5%) within the library, yet because the SH3-binding peptide appears to need to be linear they were selected for by our screening methods. Most likely they were formed during the generation of the library; one scenario is that the inserts ligated together to form head-to-head dimers and that they were subsequently cloned into m663 DNA by ligation with the vector's *Xho I* sticky end and by illegitimate ligation with the vector's *Xba I* site (see, Figure 4).

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6.5. Preparation Of Target-Coated Microtiter Wells

6.5.1. Preparation Of GST-SH3 Fusion Proteins

The preparation of Src-GST fusion protein was first described by Smith and Johnson, in Gene (1988) 67:31, the disclosure of which is incorporated by reference herein. Briefly, pGEX-derived (Pharmacia, Piscataway, NJ) constructs expressing GST fusion proteins containing the SH3 domains of Src, Grb2, Crk, Abl, or PLC γ were obtained from Dr. Channing Der (University of North Carolina at Chapel Hill); a construct expressing the SH3 domain of Yes was obtained from Dr. Marius Sudol (Rockefeller University). The use of the pGEX bacterial expression vector for the production of GST-SH3 fusion proteins is well-known to those in the art. See, e.g., Cicchetti, P. et al., in Science (1992) 257:803-806. Briefly, the coding region for a particular SH3 domain can be fused in-frame at the Bam HI site of pGEX-2T. Thus, fusion proteins were prepared as per the manufacturer's instructions, and quantified by Coomassie Blue staining of SDS-polyacrylamide gels. Microtiter wells were coated with 5-20 μ g GST-SH3 fusion protein in 100 mM NaHCO₃, pH 8.5, blocked with 100 mM NaHCO₃ (pH 8.5) 1% BSA, and washed. All washes consisted of five applications of

1XPBS, 0.1% Tween 20, 0.1% BSA (Buffer A). Where appropriate, the amount of protein bound to each well was quantified with an anti-GST antibody-based ELISA (Pharmacia, Piscataway, NJ), and with a GST-binding phage, isolated 5 during the course of this work.

6.5.2. Coating of Microtiter Wells

Bacterially expressed Src SH3 glutathione-S-transferase (Src-GST) fusion protein was purified from bacterial lysates using glutathione agarose 4B (Pharmacia), 10 according to the manufacturer's instructions. Bound Src-GST fusion protein was eluted from the glutathione agarose with 10 mM glutathione in PBS. Microtiter wells were then coated with Src-GST fusion protein (1-10 µg/well, in 50 mM NaHCO₃, pH 8.5) overnight at 4 °C. To block non-specific binding of 15 phage, 100 µL 1% BSA in 100 mM NaHCO₃, pH 8.5, was added to each well and allowed to incubate at room temperature for 1 hour. The wells were then washed five times with 200 µL PBS, 0.1% Tween 20, 0.1% BSA (Buffer A).

20 6.6. Biopanning And Subsequent Characterisation Of Phage-Displayed Random Peptide Libraries With Src-GST Fusion Protein As Target Molecule

6.6.1. Isolation of Src SH3-Binding Phage

Library screens were performed as previously described. Kay, B.K., et al., in Gene (1993) 25 128:59-65. Briefly, 1 X 10¹¹ pfu TSAR 9, TSAR 12, or R8C phage in Buffer A were incubated in a Src SH3-GST-coated well for 2 hours. The wells were washed, and bound phage were eluted with 100 µL 50 mM glycine·HCl (pH 2.2), transferred to a new well, and neutralized with 100 mL 200 mM NaHPO₄ (pH 30 7.0). Recovered phage were used to infect 1 x 10⁹ DH5αF' *E. coli* cells in 20 mL 2xYT; the infected cells were grown overnight, resulting in a 1000- to 10,000-fold amplification of phage titer. Amplified phage were panned twice more, as above, excepting the amplification step. Binding phage 35 recovered after the third round of panning were plated at a low density on a lawn of DH5αF' *E. coli* cells to yield

isolated plaques for clonal analysis. Isolated plaques were used to produce small cultures from which phage stocks and DNA were recovered for phage binding experiments and dideoxy sequencing (Sanger, F., et al., in Proc. Natl. Acad. Sci. USA 5 (1977) 74:5463-5467), respectively. Clones were confirmed as binding the SH3 domain by applying equal titers of phage to wells containing Src SH3-GST or GST alone, and titering the number of eluted particles from each well, or detecting bound phage with an anti-phage antibody-based ELISA (Pharmacia).

10 Indeed, the ability of isolated phage clones to bind to several SH3 domains derived from a variety of different proteins can be investigated by the manner described above. GST-SH3 fusion proteins containing SH3 domains from a variety of different proteins are bound to microliter wells. An 15 aliquot of the aforementioned phage stocks (50 μ L) is introduced into wells containing the different GST-SH3 fusion proteins. After room temperature incubation for 1-2 hours, the liquid contents of the microtiter plates are removed, and the wells are washed 5 times with 200 μ L Buffer A. Bound 20 phage are eluted with 100 μ L 50 mM glycine (pH 2.2), transferred to a new well, and neutralized with 100 μ L 200 mM NaHPO₄ (pH 7.0). The phage are diluted 10⁻³- to 10⁻⁶-fold, and aliquots are plated onto lawns of DH5 α F' *E. coli* cells to establish the number of plaque forming units in the output 25 sample. From these experiments, the relative specificity of different Src SH3 binding clones for SH3 domains derived from other proteins is determined.

6.6.2. Phage ELISA and Nucleotide Sequencing

30 To evaluate the binding of isolates to various targets proteins, enzyme-linked-immuno-assays (ELISA) were also performed. Bacterial cultures were infected with phage isolates and cultured overnight in 2XYT at 37 °C. The cells were spun down and 25 mL of supernatant was added to 35 microtiter plate wells coated with 50 mL of protein (1 mg/mL in 100 mM NaHCO₃, pH 8.4; overnight at 4 °C or for a few hours at room temperature) and blocked (1 mg/mL BSA in 100 mM

NaHCO₃, pH 8.4; for about one hour). The phage are incubated in the well with 25 mL of PBS-0.1% Tween 20 at RT for 2 hr. The wells are then washed multiple times over 30 minutes. To each well is added 50 µL of polyclonal anti-phage antibody conjugated to horseradish peroxidase. The antibody is diluted 1:3000 in BSA-PBS-Tween 20; it was obtained from Pharmacia (Piscataway, NJ; catalog number 27-9402-01). After 30 minutes, the wells are washed again with BSA-PBS-Tween 20 for 20 minutes. Finally, 100 µL of ABTS reagent (Pharmacia, with H₂O₂) are added to each well for the development of color. Plates are read with a plate reader (Molecular Devices, Menlo Park, CA) at 405 nm wavelength.

The nucleotide sequence of the relevant segments of the Src SH3 binding clones (or phage clones that bind to SH3 domains of other proteins) were sequenced using standard methods. Sanger, F., et al., in Proc. Natl. Acad. Sci. USA (1977) 74:5463-5467. The oligo primer 5'-AGCGTAACGATCTAAA-3' (SEQ ID NO:102) was used, which is 89 nucleotides downstream of the gene III cloning site of M13 m666. The nucleotide sequences were analyzed with the MacVector computer program (IBI, New Haven, CT, USA). From this nucleotide sequence information the primary sequence of each Src SH3 binding peptide was deduced. The corresponding synthetic peptides were then prepared by techniques well known in the art with or without flanking sequences. Indeed, these synthetic peptides have been shown to bind to SH3 domain targets, with those possessing the phage flanking amino acid residues exhibiting greater binding affinity.

6.7 In Vitro Peptide Binding Assays

Peptides were obtained from Research Genetics (Birmingham, AL), Chiron Mimotopes (Victoria, Australia), or synthesized by conventional techniques by Dr. J. Mark Carter of Cytogen Corporation (Princeton, NJ). Peptide purity was assessed by HPLC and/or mass spectrometry. Biotinylated peptides were synthesized with either a KSGSG (SEQ ID NO:103) or a GSGS (SEQ ID NO:104) peptide linker (a spacer) between

the biotin and the N-terminus of the peptide. Binding experiments were performed as above, excepting the use of 10 μ M peptide instead of phage. Bound biotinylated peptide was detected with streptavidin conjugated to alkaline phosphatase (Sigma Chemical Co., St. Louis, MO). After one hour incubation period at room temperature, the wells were washed, and a solution of 3 mM p-nitrophenyl-phosphate (US Biochemicals, Cleveland, OH) in 50 mM NaCO₃ (pH 9.8), and 50 mM MgCl₂ was added and color allowed to develop. Signals were read with an ELISA plate reader (Molecular Devices, Menlo Park, CA) at 405 nm wavelength. Binding experiments were performed in triplicate. The results are presented in Figures 7 and 8.

6.8. Peptide Competition of GST-SH3 Affinity Precipitations of Cell Lysates

Labeled proteins are prepared by incubating a culture of HeLa cells overnight with $\geq 100 \mu$ Ci/mL ³⁵S-methionine. The cells are then washed and lysed with mild detergent. This mixture of radioactive proteins is incubated with Src-GST fusion protein that has been immobilized on glutathione-linked Sepharose beads (Pharmacia, Piscataway, NJ). After several hours of tumbling, the beads are pelleted gently by low-speed centrifugation, and the supernatant is discarded. The beads are then resuspended into a slurry in PBS-0.1% Tween 20, pelleted, and washed several additional times. Finally, a 2% SDS solution is added to the sample, which is then boiled at 100 °C for 3 minutes. Afterward, the sample is centrifuged, and the supernatant loaded on a 10% polyacrylamide SDS gel for electrophoresis. After the proteins have been resolved, the gel is fixed, dried down, and exposed to X-ray film for autoradiography or phosphor plates for scanning by a Molecular Dynamics PhosphorImager.

The ability of Src SH3 to bind certain ³⁵S-labeled proteins is examined for competitiveness with exogenous peptides. Synthetic peptides corresponding to phage-displayed inserts and motifs are added at the time that the

lysate is incubated with the Src-GST fusion protein immobilized on glutathione-linked sepharose beads. The SH3 binding peptides block binding of all or some of the labeled proteins while negative control peptides (unrelated peptide sequences) do not. The amount of competition is quantified and correlated with the amount of added SH3-domain binding peptides.

Alternatively, NIH 3T3 cells were grown in Dulbecco's Modified Eagle Medium (DME) + 10% fetal calf serum (FCS) + 80 $\mu\text{Ci/mL}$ Tran³⁵S-label (ICN), washed with PBS, lysed in RIPA buffer, and pelleted. Supernatant from 1.5×10^6 cells was precleared with 100 μg glutathione-agarose-immobilized GST. The supernatant was then incubated with 10 μg glutathione-agarose-immobilized GST-SH3 fusion protein with or without added test peptide in a final volume of 250 μL . Pelleted beads were washed with 1 mL each of RIPA, RIPA + 1% deoxycholate + 0.1% SDS, and PBS, resuspended in 50 μL SDS-PAGE sample buffer, boiled, and subjected to SDS-PAGE (7.5%). Labeled proteins were detected by phosphorimaging (Molecular Dynamics). The results are presented in Figure 9.

6.9. Peptide Competition of GST-SH3 Affinity Precipitations of PI-3' Kinase From Cell Lysates

It is possible to follow the precipitation of PI-3' Kinase by Src from cell lysates in the presence or absence of SH3-binding peptides. HeLa cells are lysed with detergent and the protein mixtures are incubated for several hours with the Src-GST fusion protein immobilized on glutathione-linked Sepharose beads. After several hours of tumbling, the beads are pelleted gently by low-speed centrifugation and the supernatant is discarded. The beads are then resuspended into a slurry in PBS-0.1% Tween 20, pelleted, and washed several additional times. Finally, an SDS solution is added to the sample, which is then boiled at 100 °C for 3 minutes. Subsequently, the sample is centrifuged, and the supernatant is loaded on a 10% polyacrylamide SDS gel for electrophoresis. After the proteins have been resolved, the

gel is blotted to nitrocellulose or nylon (i.e., western blot). The filter is then probed with a PI-3' Kinase antibody (monoclonal and polyclonal antibodies are available from Upstate Biotechnology Incorporated, Lake Placid, NY) and an enzyme-linked secondary antibody. The amount of PI-3' Kinase is then quantitated.

The ability of Src SH3 to bind PI-3' Kinase is examined for competability with exogenous peptides. Synthetic peptides corresponding to phage-displayed inserts and motifs are added at the time that the lysate is incubated with the Src-GST fusion protein that has been immobilized on glutathione-linked sepharose beads. Ten-fold and one hundred-fold molar excess of peptides are used relative to SH3 proteins. The SH3 binding peptides block binding of the PI-3' Kinase as detected on western blots while negative control peptides (unrelated peptide sequences) do not. The amount of competition is quantified and correlated with the amount of added SH3-domain binding peptides.

6.10. **In Vivo Association Of SH3-Binding Peptides With SH3-Domains Of Proteins**

To demonstrate association of the SH3-binding peptides with SH3-domains of proteins inside cells, the SH3-binding peptides are tagged and localized in cells. For example, Bar-Sagi et al., in Cell (1993) 74:83-91, have shown that SH3-binding proteins localize to the cytoskeleton when expressed in cells. Thus, the SH3 domain-binding peptides of the present invention can serve as cellular targetting signals (e.g., to the cytoskeleton). Accordingly, the peptides are tagged with biotin and, subsequently, injected into cells. Alternatively, one can transfect into cells a recombinant plasmid that expresses a fusion protein comprising of the SH3-binding peptide and the green fluorescent protein (GFP, Chalfie et al., in Science (1994) 263:802-805). The location of the biotinylated peptide or the GFP fusion protein is then assayed with FITC-labeled streptavidin in paraformaldehyde-fixed cells or by direct

fluorescence in living cells, respectively. Localization of the SH3-binding peptides to the cytoskeleton demonstrates that the SH3-binding peptides can bind SH3-domain proteins *in vivo*. In addition, focal adhesions, which are rich in Src, are also sites of potential subcellular localization of SH3-binding peptides.

Thus, NIH 3T3 fibroblasts were cultured *in vitro* on glass coverslips coated with fibronectin. After two days of growth at 37 °C, the cells were fixed for one hour at room temperature in the presence of 2% paraformaldehyde (pH 7.5). The coverslips were washed with PBS-0.1% Tween 20 several times to remove the fixative. Next, the coverslips were dipped into acetone (chilled at -20 °C) for approximately 20 seconds and allowed to air-dry. The coverslips were washed again with PBS-0.1% Tween 20, containing BSA (1 mg/mL), and incubated for 2 hours at room temperature with different biotinylated peptides in PBS-0.1% Tween 20. The coverslips were washed and then incubated with 1 mg/mL streptavidin-Cy3 (Jackson ImmunoResearch Co., West Grove, PA) for 1 hour at room temperature. Finally, the coverslips were washed in PBS-0.1% Tween 20, mounted in a glycerol solution on a glass slide, and viewed with a Nikon Optiphot epifluorescence microscope and a 60x oil immersion lens.

The results are presented in Figure 11, in which panel A displays cells stained with the conjugate biotin-spacer-VLKRPLPIPPVTR (SEQ ID NO:64); panel B exhibits cells stained with the conjugate, biotin-spacer-GILAPPVPPRNTR (SEQ ID NO:63); panel C shows cells stained with the long consensus peptide, biotin-spacer-RSTPRPLPPLPTTR (SEQ ID NO:67); and panel D shows cells stained with the proline-rich vinculin peptide conjugate, biotin-spacer-LAPPKPPLPEGEV (SEQ ID NO:70). The "spacer" sequence is KSGSG (SEQ ID NO:103). As shown in Figure 11, the panels in which SH3 domain-binding peptides were used present a bright display of fluorescence activity that is in sharp contrast to the relatively "dark" features of panel D (non-SH3 domain binding vinculin segment). These results demonstrate further the ability of

the SH3 domain-binding peptides of the present invention to localize to protein targets (e.g., Src and Src-related proteins) within cells and provide an image thereof.

5 6.11. **In Vivo Modulation Of Src In Oocytes With SH3-Binding Peptides**

When *Xenopus laevis* oocytes are injected with mRNA encoding deregulated Src, there are dramatic cytological and biochemical changes in the oocyte (Unger, T.F. and Steele, R.E., in Mol. Cell. Biol. (1992) 12:5485-5498). The applicants have obtained the plasmid for generating Src mRNA, which is available from Dr. Robert Steele (University of California at Irvine). Synthetic SH3-binding peptides are injected into oocytes that have been previously injected with Src mRNA. The state of the cytoskeleton is inspected visually by observing the arrangement of cortical pigment granules under a dissecting microscope. The state of phosphorylation of several proteins is examined by western blotting with an anti-phosphotyrosine monoclonal antibody (4G10; Upstate Biotechnology Incorporated), as described in Unger and Steele, above.

 6.12. **Progesterone-induced *X. laevis* Oocyte Maturation**

Segments of adult ovary were removed surgically and incubated in 0.1% collagenase type D (Boehringer Mannheim, Indianapolis, IN) in Ca²⁺-free OR2 (82.5 mM NaCl, 2.5 mM KCl, 1.0 mM MgCl₂, 1.0 mM Na₂HPO₄, 5.0 mM HEPES, and 3.8 mM NaOH, pH 7.6). Oocytes were then washed 3-5 times with OR2 containing 1.0 mM CaCl₂ and allowed to recover in OR2 overnight at 18 °C. Stage VI oocytes were injected with 40 nL of 100 mM peptide or water. After injection, the oocytes were placed in OR2 with 2 mg/mL progesterone (Sigma, St Louis, MO) and incubated at 20 °C. Oocytes were scored at hourly time points for germinal vesicle breakdown (GVBD).

Figure 10 presents the results of this experiment. As shown by the graph, oocytes injected with the SH3 domain-binding peptide VLKRPLPIPPVTR (SEQ ID NO:64) exhibit a faster rate of progesterone-induced germinal vesicle breakdown relative to oocytes that had been injected with water or with the proline-rich vinculin peptide, LAPPKPPLPEGEV (SEQ ID NO:70). These results parallel those obtained by Unger and Steele, *supra*, who observed a gross alteration in the cortex of oocytes that had been injected with RNA encoding a deregulated Src variant ("active" Src) versus those injected with RNA encoding the wild-type Src ("cellular" Src). Also, as shown in Figure 3B of the Unger and Steele article, oocytes injected with deregulated or active Src RNA matured at a faster rate than oocytes injected with water or wild-type Src RNA.

The present results obtained with Src SH3 domain-binding peptides suggest that these peptides modulate the biochemical activity of "cellular" Src; in particular, it is proposed that at least some of the Src SH3 domain-binding peptides of the present invention upregulate the biochemical activity of "cellular" Src, which may be downregulated or inhibited in its normal state. Hence, the administration of the SH3 domain-binding peptides of the present invention can constitute a novel method of modulating the activity of Src or Src-related proteins. Specifically, certain of these peptides are able to activate Src-family proteins.

6.13. *In Vivo* Antagonism Of Src In Src Transformed Cells With SH3-Binding Peptides

The coding regions for SH3-binding peptides are cloned into vectors that direct their expression in animal cells. A bipartite gene is constructed, encoding a protein with c-myc epitope and SH3-binding peptide, which is transcribed from a strong constitutive promoter (e.g., SV40, CMV, HSV TK, calmodulin). The vector is introduced into either normal or Src-transformed cells via transfection (e.g., electroporation, calcium phosphate, liposomes, DEAE

dextran). Transfected cells express the bipartite gene transiently in culture. To create stable transformed cell lines, the vector carries a selectable marker (e.g., neomycin resistance) or transfection is performed in the presence of excess plasmid carrying a selectable marker (e.g., neomycin resistance) and cells selected for the marker. Transfected cells are stained by immunofluorescence to detect expression of the bipartite protein. The hybridoma 9E10 secretes a monoclonal antibody that is highly specific for the c-myc epitope (EQKLISEEDLN [SEQ ID NO:105]; see, Evan, G.A. et al., in Mol. Cell. Biol. (1985) 5:3610-3616). This antibody is used in immunofluorescence experiments to demonstrate that the bipartite protein is expressed inside the cells, and in some cases, localized to subcellular structures enriched in SH3 domain bearing proteins.

There are several controls used in these experiments. First, cells are transfected with vectors that do not have the SH3-binding peptide coding region. Second, normal (non-transformed) cells are transfected. Third, cells transformed by oncogenes other than Src are used in the transfection experiments. Fourth, cells are stained with other monoclonal antibodies that do not recognize the c-myc epitope.

Transfected cells are examined for any changes in cell shape, behavior, and metabolism as a consequence of expressing the SH3 binding peptides. Cell shape is examined by phase contrast microscope at several times after transfection; in particular, the flatness of the cells, their adhesion to the substrate, and the degree of cell ruffling are monitored. Cell division rates, cell migration, and contact inhibition are also observed over time. Finally, the amount of phosphorylated tyrosine in transfected cells is quantitated by phosphoaminoacid analysis and with an anti-phosphotyrosine monoclonal antibody (4G10; Upstate Biotechnology Incorporated) in western blotting experiments.

35

6.14 Preparation of PXXP Bias and Peptide Libraries

The preparation and characterization of preferred phage-displayed random peptide libraries have been described above in Sections 6.1 - 6.4.

5 Using procedures similar to those described in these sections, oligonucleotide inserts were constructed according to the schematic provided in FIG. 12. The inserts were then cloned into the mBAX vector, and the biased peptide libraries were expressed as described previously.

10 The mBAX vector was created in the Kay Laboratory by generating cloning sites in gene III of the M13mp18 vector (Messing, J. (1991). Cloning in M13 phage or how to use biology at its best. Gene 100, 3-12) in the manner of Fowlkes et al. (1992) (Biotechniques 13, 422-427). The mBAX
15 vector displays a peptide sequence at the N-terminus of the mature pIII protein that encodes the epitope for the mouse monoclonal antibody 7E11 (see, FIG. 13); it includes the stop codon TAG in the coding region, which is suppressed in *E. coli* carrying suppressor tRNA gene mutations known as *supE* or
20 *supF*. There are no other stop codons in the mBAX genome. The mBAX vector also carries a segment of the alpha fragment of β -galactosidase; bacterial cells expressing the omega fragment of β -galactosidase convert the clear XGal substrate into an insoluble blue precipitate. The plaques appear blue.

25 Recombinant mBAX molecules can be distinguished easily from non-recombinant molecules due to the TAG codon in the *Xho*I - *Xba*I segment in gene III of mBAX. When recombinants are generated by replacing the *Xho*I - *Xba*I fragment with oligonucleotides encoding random peptides, the recombinants
30 can be grown in bacteria with (i.e., DH5 α F') or without (i.e., JS5) suppressor tRNA mutant genes. On the other hand, the non-recombinant mBAX molecules fail to produce plaques on bacterial lawns where the bacteria (i.e., JS5) lack such suppressor genes. This is because in JS5, the TAG codon
35 serves as a stop codon to yield a truncated pIII molecule during translation; since pIII is an essential protein in

component of viable M13 viral particles, no plaques will form.

6.14.1 Discussion

The use of second generation or biased peptide libraries, which fix all or part of the RPLPPLP consensus motif for SH3 binding peptides and randomize flanking residues, has defined additional sequence residues exhibiting selective SH3 binding.

Tables 1-5, below, list the relevant amino acid sequences obtained from the biased peptide library for each set of SH3 domain binding peptides. The underscored amino acid residues indicate the fixed positions. Also, indicated for each set of new binders is a "consensus" sequence, which seeks to include the additional features gleaned from the new binding peptides. The symbol " ϕ " represents a hydrophobic residue.

TABLE 1 CORTACTIN SH3-BINDING PEPTIDES

		SEQ. ID NO.
20	PXXP.CORT.M1/2/3.PP	SSLLGPPVPPK <u>P</u> QTLFSFSR
	PXXP.CORT.M4.PP	SRLGEFSK <u>P</u> PI <u>P</u> QKPTWMSR
	PXXP.CORT.N2.PP	SRTERPPL <u>P</u> QRPDWLSYSSR
	PXXP.CORT.N3.PP.INC	SREPDWLC <u>P</u> NC <u>P</u> LLLRSDSR
25	PXXP.CORT.01/2/3.PP	SSSSHNSR <u>P</u> PL <u>P</u> EKPSWLSR
	PXYP.CORT.04.PP	SRLTPQSK <u>P</u> PL <u>P</u> PKPSAVSR
	CONSENSUS	KPP ϕ PxKPxW R

30

35

TABLE 2

NCK SH3-BINDING PEPTIDES

		SEQ. ID NO.	
5	PXXP.NCK.Q1/4.PP	<u>SSLGVGWKPLPPMRTASLSR</u>	114
	PXXP.NCK.Q2/3.PP.INC	<u>SSVGFA DRPRPPLRVESLSR</u>	115
	PXXP.NCK.R1.PP.INC	<u>SSAGILRPPEKPYRSFSLSR</u>	116
	PXXP.NCK.R2.PP	<u>SSPYTG DVPI PPLRGASLSR</u>	117
10	PXXP.NCK.R3.PP	<u>SSLMGSWPPV PPLRSDSLSR</u>	118
	PXXP.NCK.R4.PP	<u>SSIGEDTPPS PPTRRASLSR</u>	119
	PXXP.NCK.S1/4.PP	<u>SRSLSEVSPKPP I RSVLSR</u>	120
	PXXP.NCK.S2.PP.INC	<u>SSVSEGYS PPLPPRSTSLSR</u>	121
15	PXXP.NCK.S3.PP	<u>SSSFTLAAPT PPTRSLSLSR</u>	122
	PXXP.NCK.T1.PP	<u>SSPPYELPPRPPNRTVSLSR</u>	123
	PXXP.NCK.T2.PP	<u>SRVVDGLAPPPVRLSSLSR</u>	124
	PXXP.NCK.T3.PP.INC	<u>SSLGYSGAPVPPHRxSSLSR</u>	125
	PXXP.NCK.T4.PP	<u>SSISDYSRPPPPVRTLSLSR</u>	126
	CONSENSUS	ϕ xxxxxxPxPP ϕ RSxSL T	127

20

25

30

35

TABLE 3

ABL SH3 BINDING PEPTIDES

		SEQ. ID NO.	
5	PXXP.ABL.G1/2.PP	<u>SRGPRWSPPPVLPTSLSR</u>	128
	PXXP.ABL.G3/4.PP	<u>SSPPDYAAPAISSLWVDSR</u>	129
	PXXP.ABL.H1/3/4.PP	<u>SSPPHWAPPAPPAMSPPI SR</u>	130
	PXXP.ABL.H2.PP.INC	<u>SSDRCWECPPWPAGGQGRSR</u>	131
10	PXXP.ABL.I1/2/3.PP	<u>SSPPKFSPPPPPYWQLHASR</u>	132
	PXXP.ABL.I4.PP	<u>SSPPSFAPPAAPPRHSFGSR</u>	133
	PXXP.ABL.J1.PP	<u>SSAPKKPAPPVPMMAHVMSR</u>	134
	PXXP.ABL.J2.PP.INC	<u>SSPTYPPPPPPDTAKGASR</u>	135
15	PXXP.ABL.J3.PP.INC	<u>SSPXXXXPPPIPNSPQVLSR</u>	136
	PXXP.ABL.J4.PP	<u>SSPPTWTPPKPPGWGVVFSR</u>	137
	PXXP.ABL.L1.PP	<u>SSAPTWSPPALPNVAKYKSR</u>	138
	PXXP.ABL.L2/3.PP	<u>SSIKGPRFPVPPVPLNGVSR</u>	139
	PXXP.ABL.L4.PP	<u>SSPPAWSPPHRPVAFGSTSR</u>	140
	CONSENSUS	PPxWxPPPøP	141

20 TABLE 4

PLCG SH3-BINDING PEPTIDES

		SEQ. ID NO.	
	PXXP.PLCG.P1.PP	<u>SSMKVHNFPLPLPSYETSR</u>	142
	PXXP.PLCG.P2.PP	<u>SRVPPLVAPRPPSTLNSLSR</u>	143
25	PXXP.PLCG.PE.PP.INC	<u>SSLYWQHGPDPVVGAPQLSR</u>	144
	PXXP.PLCG.P4.PP	<u>SSHPLNSWPGGPFRRHNLSSR</u>	145

30

35

TABLE 5

SRC SH3-BINDING PEPTIDES

		SEQ. ID NO.
5	PXXP.SRC.A1.PP	<u>SSRALVRPLPPVPGTSLSR</u>
	PXXP.SRC.A2.PP	<u>SSFRALPLPPTPDNPFAGSR</u>
	PXXP.SRC.A3.PP	<u>SRDAPGSLPFRPLPPVPTSR</u>
	PXXP.SRC.A4.PP	<u>SSISQRALPPLPLMSDPASR</u>
10	PXXP.SRC.B1.PP	<u>SSPAYRPLPRLPDLSVIYSR</u>
	PXXP.SRC.B2/3/PP	<u>SSFINRRLPALPPDNSLLSR</u>
	PXXP.SRC.B4.PP	<u>SRLTGRPLPALPPFSDFSR</u>
	PXXP.SRC.C1.PP	<u>SRMKDRVLPPIPTVESAVSR</u>
	PXXP.SRC.C2.PP.INC	<u>SSLYSAIAPDPPPRNSSSSR</u>
15	PXXP.SRC.C3.PP	<u>SSLASRPLPLLNSAPGQSR</u>
	PXXP.SRC.D1.PP	<u>SSLTSRPLPDIPVRPSKSSR</u>
	PXXP.SRC.D2.PP.INC	<u>SSLKWRALPPLPETDTPYSR</u>
	PXXP.SRC.D3.PP	<u>SSNTNRLPPPTPDGLDVRSR</u>
20	PXXP.SRC.D4.PP	<u>SSLQSRPLPLPPQSSYPISR</u>
	CONSENSUS	RPLPPLP
		160

It should be apparent to one of ordinary skill that many other embodiments of the present invention can be contemplated beyond the preferred embodiments described above but which other embodiments nevertheless fall within the scope and spirit of the present invention. Hence, the present invention should not be construed to be limited to the preferred embodiments described herein, which serve only to illustrate the present invention, but only by the claims that follow.

Also, numerous references are cited throughout the specification. The complete disclosures of these references are incorporated by reference herein.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: SPARKS, ANDREW B.
KAY, BRIAN K.
THORN, JUDITH M.
QUILLIAM, LAWRENCE A.
DER, CHANNING J.
- (ii) TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF
ISOLATING AND USING SAME
- (iii) NUMBER OF SEQUENCES: 106
- 10 (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036-2711
- 15 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- 20 (viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 1101-192
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(B) TELEFAX: (212) 869-9741/8864
25 (C) TELEX: 66141 PENNIE
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- 30 (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "hydrophobic residue (such
as Pro or Leu)"
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- Xaa Pro Xaa Xaa Pro Pro Pro Xaa Xaa Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- 5 (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 1..3
(D) OTHER INFORMATION: /note= "Xaa = any residue other than Cys"
- 10 (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 6
(D) OTHER INFORMATION: /note= "X = any residue other than Cys"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8..9
(D) OTHER INFORMATION: /note= "X = any residue other than Cys"
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Xaa Xaa Xaa Pro Pro Xaa Pro Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:3:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
25 (B) LOCATION: 2
(D) OTHER INFORMATION: /note= "X tends to be hydrophobic"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8..9
(D) OTHER INFORMATION: /note= "X tends to be hydrophobic"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
- 30 Arg Xaa Leu Pro Pro Arg Pro Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Lys Leu Pro Pro Arg Pro Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:5:

5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10

Val Pro Pro Pro Val Pro Pro Arg Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "tends to be Pro"

20

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /note= "hydrophobic residue"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "tends to be Pro"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Xaa Xaa Pro Xaa Xaa Pro
1 5

30 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "X = any residue other than Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modifi d-site
- (B) LOCATION: 8..9
- (D) OTHER INFORMATION: /note= "X = any residu oth r than Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5

Arg Xaa Leu Pro Pro Arg Pro Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "hydrophobic residue"

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Xaa Leu Pro Pro Leu Pro Arg Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:9:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

25

Arg Pro Leu Pro Pro Leu Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "any residue other than Cys"

35

(ix) FEATURE:

- (A) NAME/KEY: Modifi d-sit
- (B) LOCATI N: 5..6
- (D) OTHER INFORMATION: /note= "any hydrophobic residue"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "any hydrophilic residue
 except Cys"

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
Arg Xaa Leu Pro Xaa Xaa Pro Xaa Xaa
1 5

10 (2) INFORMATION FOR SEQ ID NO:11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
Arg Pro Leu Pro Pro Leu Pro Thr Ser
1 5

15 (2) INFORMATION FOR SEQ ID NO:12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE:
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
Xaa Xaa Xaa Xaa
1

25 (2) INFORMATION FOR SEQ ID NO:13:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide
 (v) FRAGMENT TYPE:
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
Xaa Xaa Xaa Xaa Xaa
1 5

35 (2) INFORMATION FOR SEQ ID NO:14:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5 Xaa Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1..3
(D) OTHER INFORMATION: /note= "any residue other than Cys"

15 (ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "any residue other than Cys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 8..9
(D) OTHER INFORMATION: /note= "any hydrophobic residue"

20 (ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 11..13
(D) OTHER INFORMATION: /note= "any residue other than Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

25 Xaa Xaa Xaa Arg Xaa Leu Pro Xaa Xaa Pro Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

35 Xaa Xaa Xaa Xaa Pro Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Arg

35

40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGCTCGAGNN NBNNBNNBNN BNNBNNBNNB NNBNNBNNBN NBNNBNNBNN BNNBNNBNNB 60
NNBCCAGGT 69

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGTCCANNVN NVNNVNNVNN VNNVNNVNNV NNVNNVNNVN NVNNVNNVNN VNNVNNVNNV 60
AGATCTGG 68

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCGAGNNBN NBNNBNNBNN BNNBNNBNNB NNBNNBNNBN NBNNBNNBNN BNNBNNBNNB 60
CCAGGT 66

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCCANNVN NVNNVNNVNN VNNVNNVNNV NNVNNVNNVN NVNNVNNVNN VNNVNNVNNV
AGATC

60

65

(2) INFORMATION FOR SEQ ID NO:21:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

- 10 (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /note= "Arg or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
15 Xaa Xaa Xaa Xaa Pro Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Arg Pro Ser Arg Thr
35 40 45

(2) INFORMATION FOR SEQ ID NO:22:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 Ser His Ser Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Arg Pro Ser Arg
35 40 45
30 Thr

(2) INFORMATION FOR SEQ ID NO:23:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Ser or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /note= "Ser, Arg, Gly, Cys or Trp"

5

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Val, Ala, Asp, Glu or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

10 Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

20 TTTTGTGAC NNNBNNBNNB NNBNNBNNBN NBNBNNBNN BNGCGGTG

48

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCCACNVNN VNNVNNVNNV NNVNNVNNVN NVNNVNNVTG ATCATTTT

48

30 (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGCCACNVNN VNNVNNVNNV NNVNNVNNVN NVNNVNNVTG ATC

43

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

5

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCGACNNNNBN NBNNBNNBNN BNNBNNBNNB NNBNNBNGCG GTG

43

(2) INFORMATION FOR SEQ ID NO:28:

10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (v) FRAGMENT TYPE:

15

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION: /note= "Ser or Thr"

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 13
 - (D) OTHER INFORMATION: /note= "Ser, Arg, Gly, Cys or Trp"

20

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 15
 - (D) OTHER INFORMATION: /note= "Val, Ala, Asp, Glu or Gly"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

25

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Pro Ser Arg Thr
 20 25 30

(2) INFORMATION FOR SEQ ID NO:29:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "Ser or Thr"

35

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site

- (B) LOCATION: 16
(D) OTHER INFORMATION: /not = "Ser, Arg, Gly, Cys or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 18
(D) OTHER INFORMATION: /note= "Val, Ala, Asp, Glu or Gly"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser His Ser Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Pro Ser
20 25 30

10

Arg Thr

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

20

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(E) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGACGGCTCG AGTTGTNNKN NKNNKNNKNN KNNKNNKNNK TGTGGATCTA GAAGGATC

58

30

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCTAGATCTT CCTAG

15

(2) INFORMATION FOR SEQ ID NO:33:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

10 TCGAGTTGTN NKNNKNNKNN KNNKNNKNNK NNKTGTGGAT

40

(2) INFORMATION FOR SEQ ID NO:34:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAACANNMNN MNNMNNMNNM NNMNNMNNMA CACCTAGATC

40

(2) INFORMATION FOR SEQ ID NO:35:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser Ser Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Gly Ser Arg Pro
 1 5 10 15

Ser Arg Thr

30 (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Ser Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Gly Ser Arg Ser
 1 5 10 15

Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Thr Arg
20 25

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCGAGTTGTN NKNNKNNKNN KNNKNNKNNK NNKTGTGGAT CTAGATCCAC AVNNVNNVNN 60
VNNVNNVNNV NNVNNACAAC 80

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Ser Phe Asp Gln Gln Asp Trp Asp Tyr Ser Ile Ala Glu Lys Met
1 5 10 15
His Pro Ile Arg Pro Gly Phe Arg Glu Leu Pro Pro Leu Pro Pro Ser
20 25 30
Arg Ala Ser Phe Gly Gly Gly Ala Ser Arg Pro Ser Arg
35 40 45

25 (2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Thr Asn Val Trp Val Thr Gly Ser Val Ile Ala Arg Gly Ala Gln
1 5 10 15
Ser Arg Pro Leu Pro Ile Pro Pro Glu Thr Arg Pro Ser Arg
20 25 30

35 (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

5 Ser Thr Ala Pro Trp Gly Leu Arg Val Ala His Glu Gly Gly Val Leu
1 5 10 15
Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg Pro Ser Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:41:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

15 Ser Ser Ser Gly Tyr Val Val Pro Lys Arg Leu Gly Asp Met Arg Glu
1 5 10 15
Tyr Asn Ala His Pro Gly Leu His Val Pro Pro Asn Ser Pro Leu Pro
20 25 30
Pro Leu Pro Thr His Leu Gln Ser Ser Arg Pro Ser Arg
35 40 45

20 (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Ser Arg Gly Glu Gly Asn Asn Ile Ile Ser Ser Arg Pro Phe Leu
1 5 10 15
Ser Asn Ser Asp Pro Gly Val Ser Asn Lys Leu Thr Gly Arg Gly Pro
20 25 30
Leu Pro Pro Leu Pro Asn Asp Ser Arg Pro Ser Arg
35 40

30

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Thr Ala Val Ser Phe Arg Phe Met Pro Gly Gly Gly Gly Ala Phe
 1 5 10 15
 Tyr Ser Thr Arg Pro Val Pro Pro Ile Thr Arg Pro Ser Arg Thr
 20 25 30

5 (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Thr Ala His Ser Leu Trp Asp Trp Gly Thr Phe Ser Gly Val Ser
 1 5 10 15
 His Lys Ser Arg Leu Pro Pro Leu Pro Thr Arg Pro Ser Arg Thr
 20 25 30

15

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Pro Gly Tyr Ala Arg Ile Val Ser Tyr Arg Phe Arg Ala Leu Pro Ser
 1 5 10 15
 Pro Pro Ser Ala Ser Arg Pro Ser Arg
 20 25

25

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ser Thr Asn Asp Val Asp Trp Met His Met Trp Asn Ser Gly Gly Pro
 1 5 10 15
 His Arg Arg Leu Pro Pro Thr Pro Ala Thr Arg Pro Ser Arg
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Ser Asp Asn Trp Ala Arg Arg Val His Ala Ser Glu Leu Ile Tyr
 1 5 10 15
 Thr Asp Leu Ser Pro Gly Ile Leu Leu Ala Gln Arg Gln Leu Pro Pro
 20 25 30
 Thr Pro Gly Arg Asp Pro Ser His Ser Arg Pro Ser Arg
 35 40 45

10

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Ser Glu Ser Pro Leu Met Tyr Asn Arg Val Gly Ala Leu Gln Ser
 1 5 10 15
 Leu Thr Ser Val Pro Gly Ser Met Met His Phe Ala Leu Gln Arg Arg
 20 25 30
 Leu Pro Arg Thr Pro Pro Pro Ala Ser Arg Pro Ser Arg
 35 40 45

20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Thr Arg Trp Ser His Ser Trp Pro Gly Tyr Val Gly Gly Ala Asn
 1 5 10 15
 Pro Ser Pro Ala Thr Arg Pro Leu Pro Thr Arg Pro Ser Arg Thr Val
 20 25 30
 Glu Ser Cys
 35

30

35 (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

5 Ser Arg Tyr Asn Asp Leu Gly Thr Arg Pro Val Ser Glu Val Ile Lys
1 5 10 15
Tyr Asp Tyr Phe Pro Gly Tyr Ser Gln His Val Ile Thr Pro Asp Gly
20 25 30
Ser Tyr Ser Thr Arg Pro Leu Pro Ser Arg Pro Ser Arg Thr Val Glu
35 40 45
Ser Cys
50

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

15 Pro Gly Arg Leu Leu Leu Pro Ser Glu Pro Arg Thr Phe Tyr Asn Tyr
1 5 10 15
Gly His Asp Ser Arg Pro Ser Arg
20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

25 Ser Thr Met Tyr Gly Val Ser Trp Leu Ser Ser Gly Ser Gly Gly Ile
1 5 10 15
Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg Pro Ser Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser Ser Cys Thr Glu Lys Thr Val Ser Gly Trp Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Pro Leu Pro Il Leu Pro Arg Thr Thr Arg Pro Ser Arg
 20 25 30

5 (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ser Ser Cys Met Leu Pro Thr Asp Gly Trp Gln Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Pro Arg Pro Leu Pro Met Leu Pro Thr Thr Arg Pro Ser Arg
 20 25 30

15 (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ser Ser Cys Asp Gly Thr Gln Phe Arg Leu Asn Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Asn Arg Pro Leu Pro Met Ile Pro Thr Thr Arg Pro Ser Arg
 20 25 30

25 (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Ser Cys Met Gln Gly Gln Ala Gly Leu Lys Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Pro Leu Pro Ser Leu Pro Ile Thr Thr Arg Pro Ser Arg
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ser Ser Cys Tyr Arg Glu Lys Asp Thr Trp Gly Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Ser Arg Pro Leu Pro Ser Leu Pro Thr Thr Arg Pro Ser Arg
 20 25 30

10 (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ser Ser Cys Leu Phe Glu Gln Gly Ala Gly Thr Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Ser Leu Pro Pro Leu Pro Pro Thr Thr Arg Pro Ser Ser Arg
 20 25 30

20 (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser Ser Cys Asp Thr Gly Arg Ile Ala Pro Gly Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Pro Arg Pro Leu Pro Leu Ile Pro Thr Thr Pro Arg Ser Thr Asn
 20 25 30
 Leu Asn Leu Thr Ser Thr Thr Thr Arg Pro Ser Arg
 35 40

(2) INFORMATION FOR SEQ ID NO:60:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ser Ser Cys Gly Leu Asp Asn Ala Ala Lys Thr Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Pro Leu Pro Pro Thr Pro Leu Thr Thr Arg Pro Ser Arg
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser Ser Cys Ser Arg Ala His Glu Thr Glu Met Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Pro Gln Pro Pro Pro Pro Ile Thr Thr Arg Pro Ser Arg
 20 25 30

15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg Ser Thr Pro Arg Pro Leu Pro Met Leu Pro Thr Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:63:

25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:64:

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Val L u Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg
1 5 10

5 (2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gly Pro His Arg Arg Leu Pro Pro Thr Pro Ala Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:66:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

20 Ala Asn Pro Ser Pro Ala Thr Arg Pro Leu Pro Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

30 Arg Ser Thr Pro Arg Pro Leu Pro Pro Leu Pro Thr Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Gly Thr Val Glu Pro Val Pro Pro Pr Val Pro Pro Arg Arg Arg Pro
 1 5 10 15
 Glu Ser Ala

(2) INFORMATION FOR SEQ ID NO:69:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

10

Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro
 1 5 10 15
 Val

(2) INFORMATION FOR SEQ ID NO:70:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

20

Leu Ala Pro Pro Lys Pro Pro Leu Pro Glu Gly Glu Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "any residue other than Cys"

(ix) FEATURE:

30

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 5..6
 (D) OTHER INFORMATION: /note= "any hydrophobic residue"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Arg Xaa Leu Pro Xaa Xaa Pro
 1 5

35

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

5 Pro Gly Phe Arg Glu Leu Pro Pro Leu Pro Pro Ser Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala Gln Ser Arg Pro Leu Pro Ile Pro Pro Glu Thr Arg
1 5 10

15

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Pro Pro Asn Ser Pro Leu Pro Pro Leu Pro Thr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

30

Thr Gly Arg Gly Pro Leu Pro Pro Leu Pro Asn Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr S r Thr Arg Pro Val Pro Pro Ile Thr Arg Pr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

10

Ser His Lys Ser Arg Leu Pro Pro Leu Pro Thr Arg Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Tyr Arg Phe Arg Ala Leu Pro Ser Pro Pro Ser Ala Ser
1 5 10

20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Leu Ala Gln Arg Gln Leu Pro Pro Thr Pro Gly Arg Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:80:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

35

Ala L u Gln Arg Arg L u Pr Arg Thr Pro Pro Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Pro Ala Thr Arg Pro Leu Pro Thr Arg Pro Ser Arg Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:82:

10

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

15

Tyr Ser Thr Arg Pro Leu Pro Ser Arg Pro Ser Arg Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:83:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

25

Xaa Pro Gly Arg Ile Leu Leu Leu Pro Ser Glu Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ser Gly Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn
1 5 10

35 (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

5 Arg Ser Thr Arg Pro Leu Pro Ile Leu Pro Arg Thr Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

 Ser Thr Pro Arg Pro Leu Pro Met Leu Pro Thr Thr Arg
 1 5 10

15

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

 Ser Thr Asn Arg Pro Leu Pro Met Ile Pro Thr Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:88:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

30

 Arg Ser Thr Arg Pro Leu Pro Ser Leu Pro Ile Thr Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Ser Thr S r Arg Pro Leu Pro Ser Leu Pro Thr Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:90:

5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

10

Arg Ser Thr Arg Pro Leu Pro Ser Leu Pro Ile Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:91:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

20

Arg Ser Thr Arg Gln Leu Pro Ile Pro Pro Thr Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:92:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Ser Thr Pro Arg Pro Leu Pro Leu Ile Pro Thr Thr Pro
1 5 10

30

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Arg Ser Thr Arg Pro Leu Pro Pr Thr Pr Leu Thr Thr

1

5

10

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Arg Ser Thr Arg Pro Gln Pro Pro Pro Ile Thr Thr
1 5 10

10

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Arg Pro Leu Pro Met Leu Pro
1 5

15

20 (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "Pro or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Arg Pro Leu Pro Xaa Leu Pro
1 5

30

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

35

Arg Ser Thr Pro
1

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Arg Ser Thr Pro Ala Pro Pro Val Pro Pro Arg Thr Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AGCGTAACGA TCTCCCG

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TTCACCTCGA AAGCAAGCTG

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CCTCATAGTT AGCGTAACG

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear

5

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AGCGTAACGA TCTAAA

16

10 (2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Lys Ser Gly Ser Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:104:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

25 Gly Ser Gly Ser
 1

(2) INFORMATION FOR SEQ ID NO:105:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 1 5 10

35

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

5 Ser Ser Cys Asp His Thr Leu Gly Leu Gly Trp Cys Gly Ser Arg Ser
1 5 10 15
Thr Arg Gln Leu Pro Ile Pro Pro Thr Thr Thr Arg Pro Ser Arg
20 25 30

10

15

20

25

30

35

WHAT IS CLAIMED IS:

1. A peptide having at least nine and up to forty-five amino acid residues, including an amino acid sequence of the formula, R-2-L-P-5-6-P-8-9 (SEQ ID NO:10), positioned
5 anywhere along the peptide, in which each number represents an amino acid residue, such that 2 represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, 8 represents any amino acid
10 residue except cysteine, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src, provided that said peptide is not R-P-L-P-P-L-P-T-S (SEQ ID NO:11).
- 15 2. The peptide of claim 1 in which 2 is a P, R, A, L, Q, E or S.
3. The peptide of claim 1 in which 5 is a P, M, I or L.
4. The peptide of claim 1 in which 6 is a P, L, I or
20 V.
5. The peptide of claim 1 in which 8 is a T, R, P, I, N, E, V, S, A, G or L.
6. The peptide of claim 1 in which 9 is a T, R, S, H or D.
- 25 7. The peptide of claim 1 which further comprises a C-terminal-flanking amino acid sequence of the formula 10, 10-11, 10-11-12, 10-11-12-13 (SEQ ID NO:12) or 10-11-12-13-14 (SEQ ID NO:13), in which each number represents any amino acid residue except cysteine, such that 10 is bound to 9 by a
30 peptide bond.
8. The peptide of claim 7 in which 10 is T, R, L, S, D, P, A or N.
9. The peptide of claim 7 in which 11 is R, P, A, Q, S or T.
- 35 10. The peptide of claim 7 in which 12 is P, S, R or T.
11. The peptide of claim 7 in which 13 is P, S, R, F, H or T.

12. The peptide of claim 7 in which 14 is S, R, G or T.
13. The peptide of claim 1 which further comprises an N-terminal-flanking amino acid sequence of the formula 1', 2'-1', 3'-2'-1' or 4'-3'-2'-1' (SEQ ID NO:14) in which each number represents any amino acid residue except cysteine, such that 1' is bound to R by a peptide bond.
14. The peptide of claim 13 in which 1' is T, P, S, N, F, W, K, H, Q or G.
15. The peptide of claim 13 in which 2' is S, T, G, P, R, Q, L, A or H.
16. The peptide of claim 13 in which 3' is R, S, P, G, A, V, Y or L.
17. The peptide of claim 13 in which 4' is R, S, V, T, G, L or F.
18. A peptide having at least thirteen and up to forty-five amino acid residues, including an amino acid sequence of the formula, 3'-2'-1'-R-2-L-P-5-6-P-8-9-10 (SEQ ID NO:15), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 3', 2', 1', 2, 8, and 10 each represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src.
19. The peptide of claim 18 in which 5 is a P or M.
20. The peptide of claim 18 in which 1' is T, P, S or N.
21. The peptide of claim 18 in which 2' is S or T.
22. The peptide of claim 18 in which 3' is R or S.
23. The peptide of claim 18 in which 10 is T or R.
24. The peptide of claim 1 the binding affinity of which is at least three-fold greater than that exhibited by the peptide RPLPPLP for the SH3 domain of Src.
25. The peptide of claim 18 the binding affinity of which is at least three-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9) for the SH3 domain of Src.

26. The peptide of claim 1 the binding affinity of which is at least four-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9) for the SH3 domain of Src.

27. The peptide of claim 18 the binding affinity of which is at least four-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9) for the SH3 domain of Src.

28. The peptide of claim 1 which further exhibits a general binding affinity for the SH3 domain of Abl, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, p85 PI-3'Kinase, and proteins related thereto.

29. The peptide of claim 1 which exhibits a selective binding affinity for the SH3 domain of Src and Src-related proteins.

30. The peptide of claim 18 which further exhibits a general binding affinity for the SH3 domain of Abl, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, p85 PI-3'Kinase, and proteins related thereto.

31. The peptide of claim 18 which exhibits a selective binding affinity for the SH3 domain of Src and Src-related proteins.

32. A peptide having the amino acid sequence RSTPRPLPMLPTTR (SEQ ID NO:62).

33. A peptide having the amino acid sequence RSTPRPLPPLPTTR (SEQ ID NO:67).

34. A peptide having the amino acid sequence GILAPPVPPRNTR (SEQ ID NO:63).

35. A peptide having the amino acid sequence VLKRPLPIPPVTR (SEQ ID NO:64).

36. A peptide having the amino acid sequence GPHRRLPPTPATR (SEQ ID NO:65).

37. A peptide having the amino acid sequence ANSPATRPLPTR (SEQ ID NO:66).

38. A peptide having an amino acid sequence selected from the group consisting of RSTRPLPILPRTT, STPRPLPMLPTTR, STNRPLPMIPTTR, RSTRPLPSLPITT, STSRPLPSLPPTTR, RSTRSLPPLPPTT, RSTRQLPIPPPTT, STPRPLPLIPTTP, RSTRPLPPTPLTT, and RSTRPQPPPPITT (SEQ ID NOS:85-94).

39. A peptide having the amino acid sequence selected from the group consisting of VLKRPLPIPPVTR (SEQ ID NO:64), YSTRPVPPITRPS (SEQ ID NO:76), SHKSRLPPLPTRP (SEQ ID NO:77), GPHRRLPPTPATR (SEQ ID NO:65), PATRPLPTRPSRT (SEQ ID NO:81), 5 and SGGILAPPVPPRN (SEQ ID NO:84).

40. A peptide having the amino acid sequence selected from the group consisting of PPNSPLPPLPTH (SEQ ID NO:72), TGRGPLPPLPND (SEQ ID NO:74), YRFRALPSPPSAS, LAQRQLPPTPGRD ALQRRLPRTPPPA (SEQ ID NOS:78-80), YSTRPLPSRPSRT, and 10 XPGRIILLPSEPR (SEQ ID NOS:82-83).

41. A construct comprising a nucleic acid encoding a peptide of claim 1 or its complement.

42. The construct of claim 41 which is a DNA polynucleotide.

15 43. The construct of claim 41 which is a RNA polynucleotide.

44. A construct comprising a nucleic acid encoding a peptide of claim 18 or its complement.

45. The construct of claim 44 which is a DNA 20 polynucleotide.

46. The construct of claim 44 which is a RNA polynucleotide.

47. The construct of claim 41 which is a transforming vector.

25 48. The construct of claim 44 which is a transforming vector.

49. A host cell transformed with the vector of claim 47.

50. A host cell transformed with the vector of claim 30 48.

51. A conjugate comprising a peptide of claim 1 and a second molecule.

52. The conjugate of claim 51 in which said second molecule is selected from the group consisting of an amino 35 acid, a peptide, a protein, a nucleic acid, a nucleoside, a glycosidic residue, a label, a drug or a small molecule.

53. A diagnostic kit for the detection of SH3 domains comprising an SH3 domain-binding peptide and a detectable label conjugated to said peptide directly, indirectly or by complexation, said peptide comprising: (i) a core sequence motif of the formula RXLP $\phi\phi$ P (SEQ ID NO:71), wherein X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue, each letter representing the standard one-letter designation for the corresponding amino acid residue; and (ii) two or more additional amino acid residues flanking said core sequence at its C-terminal end, N-terminal end or both.

54. A drug delivery system comprising an SH3 domain-binding peptide and a drug conjugated to said peptide directly, indirectly or by complexation, said peptide comprising: (i) a core sequence motif of the formula RXLP $\phi\phi$ P (SEQ ID NO:71), wherein X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue, each letter representing the standard one-letter designation for the corresponding amino acid residue; and (ii) two or more additional amino acid residues flanking said core sequence at its C-terminal end, N-terminal end or both.

55. The drug delivery system of claim 54 which may be administered parenterally, orally, enterally, topically or by inhalation.

56. The drug delivery system of claim 54 which may be administered intranasally, ophthalmically or intravaginally.

57. The drug delivery system of claim 54 which is in the form of a solid, gel, liquid or aerosol.

58. A method of modulating the activity of Src or Src-related proteins comprising administering a composition comprising an effective amount of a peptide of claim 1 and a carrier.

59. The method of claim 58 which inhibits the activity of Src or Src-related proteins.

60. The method of claim 58 which activates Src or Src-related proteins.

61. A method of identifying a peptide having a region that binds to an SH3 domain comprising:

- (a) providing an immobilized target protein comprising an SH3 domain;
- 5 (b) incubating said immobilized target protein with an aliquot taken from a random peptide library;
- (c) washing unbound peptide from said immobilized target protein;
- (d) recovering the peptide bound to said
10 immobilized target protein; and
- (e) determining the primary sequence of the SH3 domain-binding peptide.

62. The method of claim 61 in which said library is a displayed random peptide library.

- 15 63. The method of claim 62 in which said library is a phage-displayed random peptide library.

64. The method of claim 62 in which said library is a phagemid-displayed random peptide library.

- 20 65. The method of claim 61 in which step (c) includes washing unbound phage from said immobilized target protein; step (d) includes recovering the phage bound to said immobilized target protein; and step (e) includes determining the relevant nucleotide sequence of said binding phage nucleic acid, from which the primary sequence corresponding
25 to the SH3 domain-binding peptide is deduced.

66. A method of identifying a peptide having a region that binds to an SH3 domain comprising:

- (a) providing an immobilized target protein comprising an SH3 domain;
- 30 (b) incubating said immobilized target protein with an aliquot taken from a phage-displayed random peptide library, which library includes peptides having a random sequence of ≥ 8 amino acid residues;
- (c) washing unbound phage from said immobilized
35 target protein;
- (d) recovering the phage bound to said immobilized target protein; and

() determining the relevant nucleotide sequence of said binding phage nucleic acid and deducing the primary sequence corresponding to the SH3 domain-binding peptide.

67. The method of claim 66 which further comprises
5 amplifying the titer of the recovered phage.

68. The method of claim 66 which further comprises repeating the steps of incubation, washing and recovery to provide SH3 domain-binding peptide-enriched phage.

69. A pharmaceutical composition comprising an SH3
10 domain-binding peptide and a pharmaceutically acceptable carrier, said peptide comprising: (i) a 9-mer sequence motif of the formula RXLP ϕ ϕ PX ψ (SEQ ID NO:10), wherein X represents any amino acid except cysteine, ϕ represents a hydrophobic amino acid residue, and wherein ψ is a hydrophilic amino acid
15 residue except cysteine, each letter representing the standard one-letter designation for the corresponding amino acid residue; and, optionally, (ii) additional amino acid residues flanking said 9-mer sequence at its C-terminal end, N-terminal end or both, up to a total of 45 amino acid
20 residues, including said 9-mer sequence.

70. The composition of claim 69 in which at least one additional amino acid flanks said 9-mer sequence.

71. The composition of claim 69 in which at least two additional amino acids flank said 9-mer sequence.

25 72. The composition of claim 69 in which at least three additional amino acids flank said 9-mer sequence.

73. A method of disrupting protein tyrosine kinase-mediated signal transduction pathways comprising administering an effective amount of a peptide of claim 1.

30 74. A method of regulating the processing, trafficking or translation of RNA by administering an effective amount of a peptide of claim 1.

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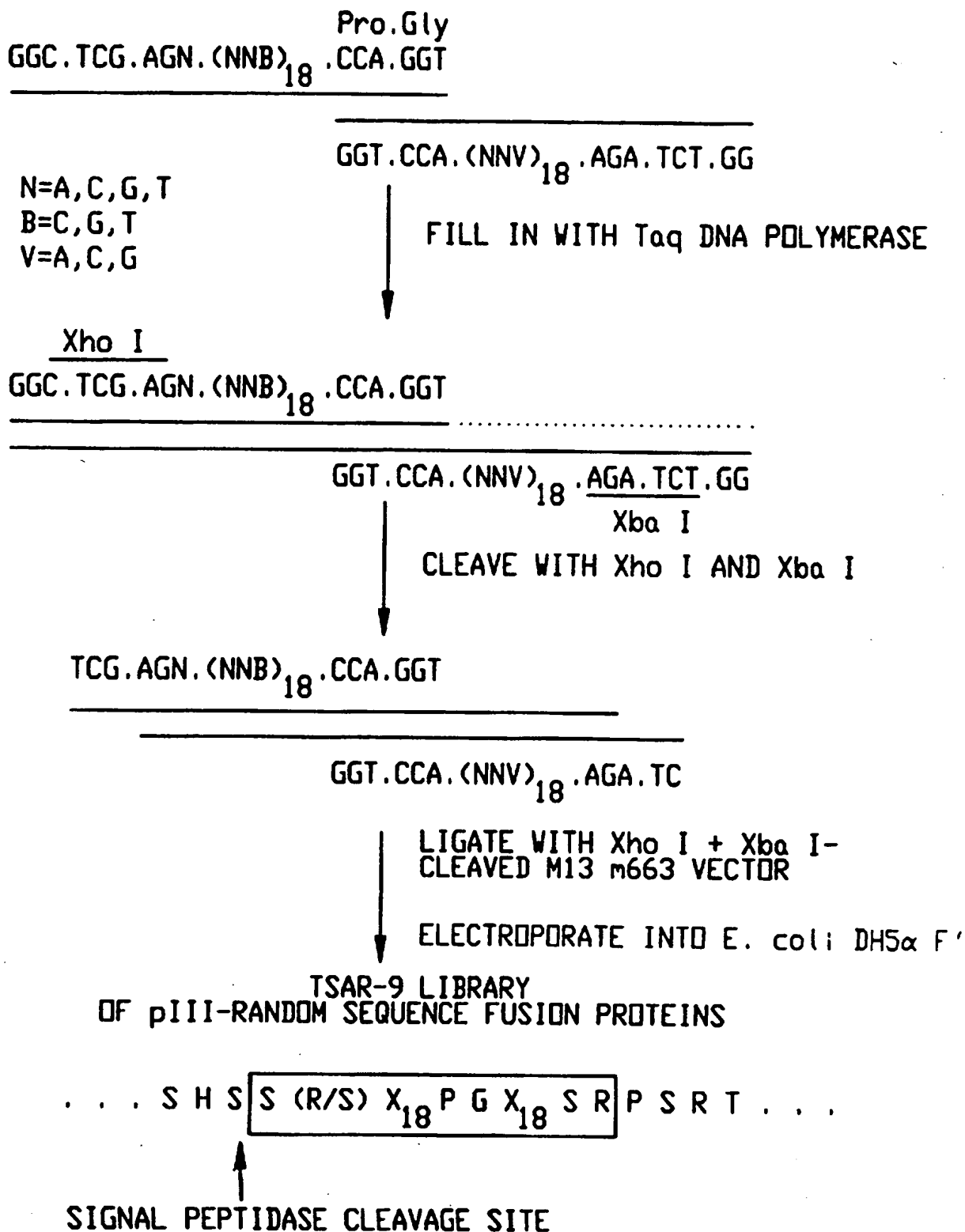


FIG.1

SUBSTITUTE SHEET (RULE 26)

2/14

Gly

tt.ttg.tcg.acN.(NNB)₁₀.Ngc.ggt.g

N=A,G,T,C

B=G,T,C

V=G,A,C

cg.cca.cNV.(NNV)₁₀.tga.tca.ttt.t

FILL IN WITH Taq DNA POLYMERASE

Sal I

tt.ttg.tcg.acN.(NNB)₁₀.Ngc.ggt.g

cg.cca.cNV.(NNV)₁₀.tga.tca.ttt.t

Spe I

CLEAVE WITH Sal I + Spe I

tcg.acN.(NNB)₁₀.Ngc.ggt.g

cg.cca.cNV.(NNV)₁₀.tga.tc

LIGATE WITH Xho I + Xba I -
CLEAVED M13 m663 VECTOR

ELECTROPORATE INTO E. coli DH5α F'

TSAR-12 LIBRARY
OF pIII-RANDOM SEQUENCE FUSION PROTEINS

... S H S S (S/T) X₁₀ ϕ G θ X₁₀ T R P S R T ...

ϕ=S,R,G,C, OR W

θ=V,A,D,E, OR G

SIGNAL PEPTIDASE CLEAVAGE SITE

FIG.2

SUBSTITUTE SHEET (RULE 26)

3/14

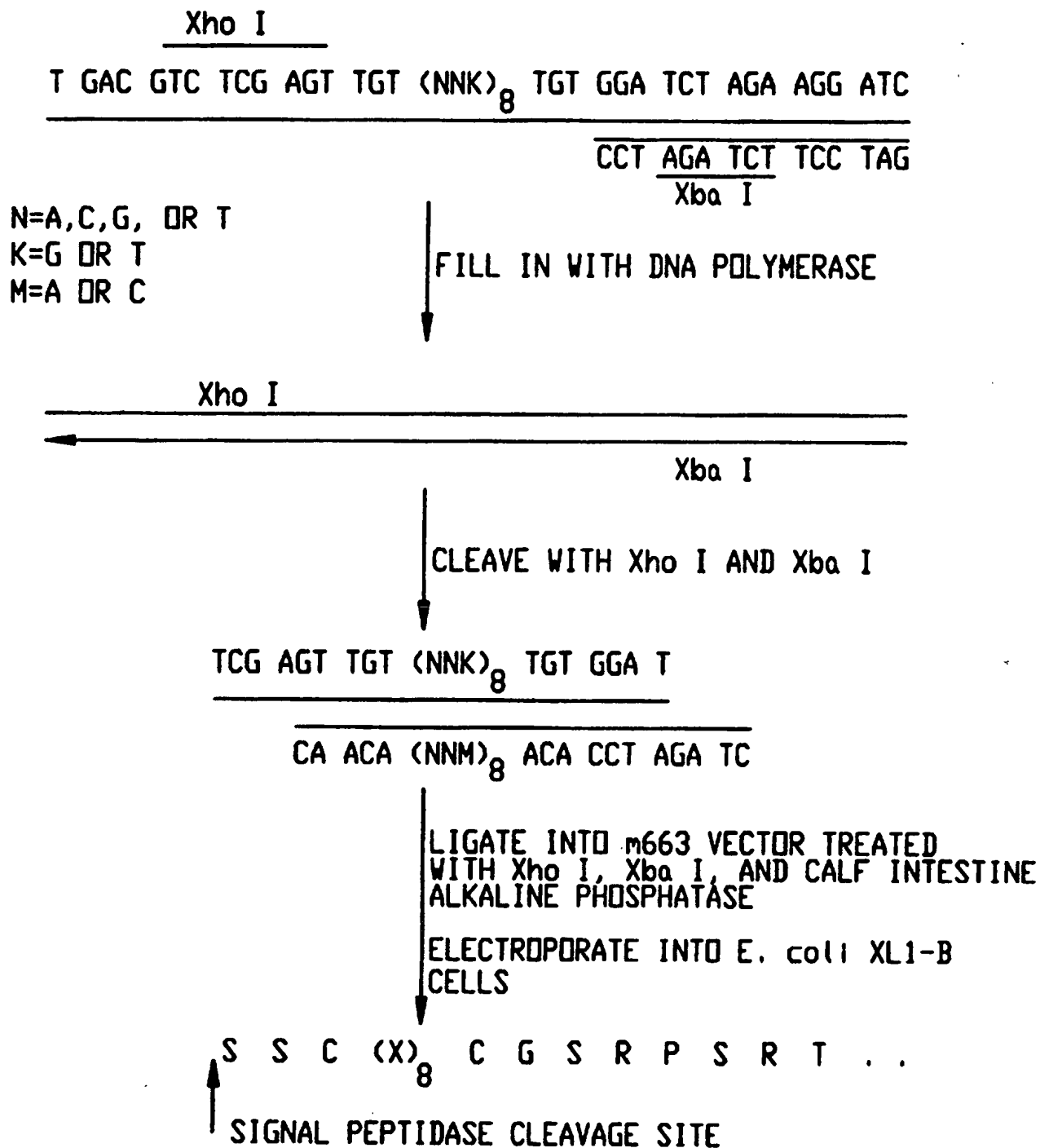


FIG.3

SUBSTITUTE SHEET (RULE 26)

4 / 14

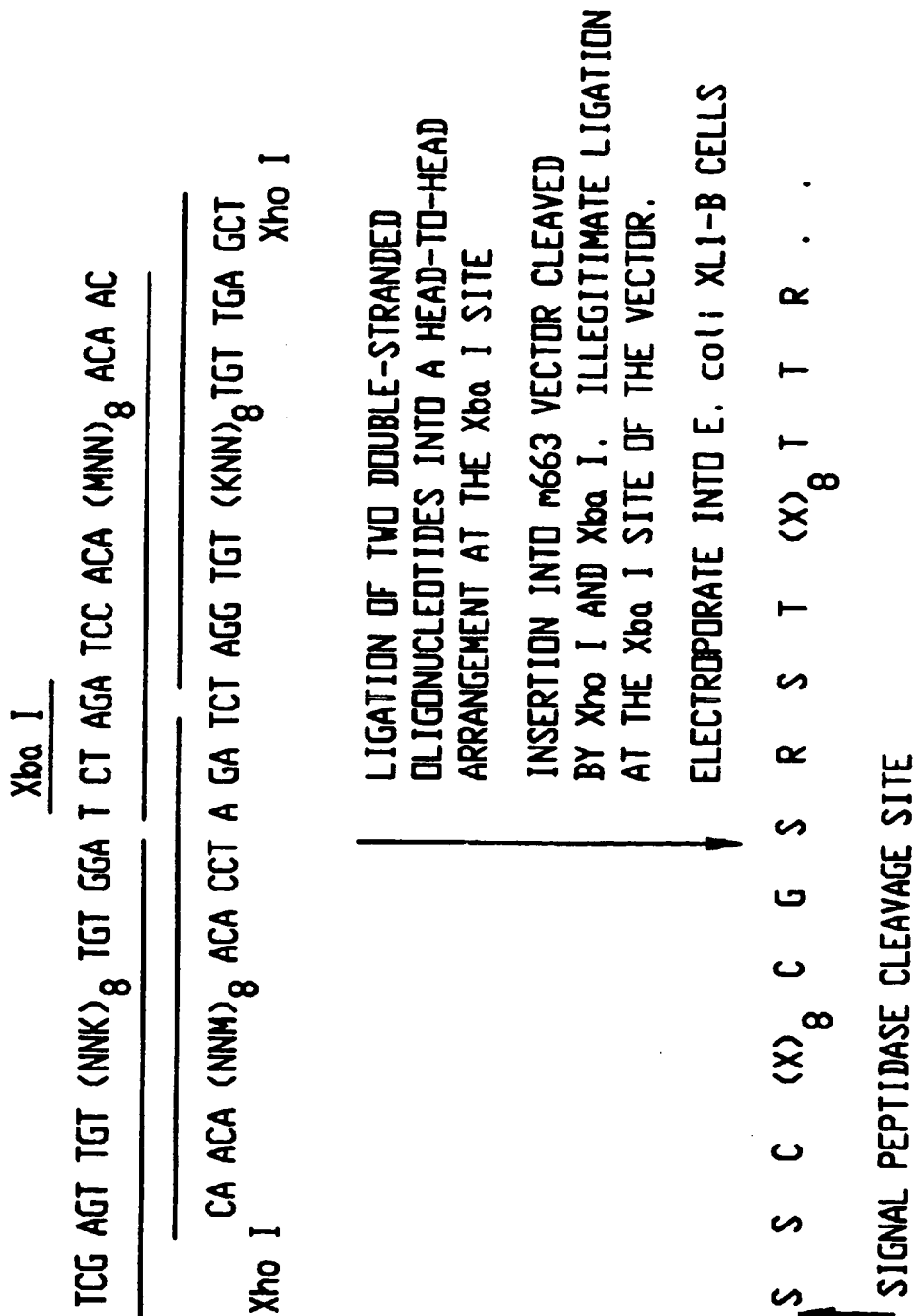


FIG.4

CLONE	SEQUENCE	FREQUENCY
T9.SRC3.2	SSFDQQDDVDSIAEKMHPIRPGF	2
T12.SRC3.4	STNVVVTGSVIARGAQS	1
T12.SRC3.6	STAPVGLRVAHEGGVLK	1
T9.SRC3.4	SSSGYVVPKRLGDMREYNAPGLHVPPN	1
T9.SRC3.6	SSRGEGNNIISSRPFLSNSDPGVSNKL TGR	2
T12.SRC3.7	STAVSFRFMPGGGAFYST	1
T12.SRC3.5	STAHSLVDVGTFSGVSHKS	1
T9.SRC3.7	XPGYARIVSYRF	1
T12.SRC3.3	STNDVDVTHMWNSSGPH	1
T9.SRC3.5	SSDNVARRYHASELIYTDLSPGILLAQ	4
T9.SRC3.1	SSESPLMYNRVGALQSLTSVPGSMHFAIQ	1
T12.SRC3.2	STRVSHSVPGYVGANPSPAT	5
T9.SRC3.3	SRYNDLGTRPVSE'IKYDYFPGYSQHVI TPDGSYST	19
T9.SRC3.8	XPG	2
T12.SRC3.1	STMYGVSVLSSGSGGILA	1
	Consensus	25
	RPLPPLP	
	RELPLP	
	RPLPIPP	
	RPLPIPP	
	SPLPPLP	
	GPLPPLP	
	RPVPPIT	
	RLPPLPT	
	RALPSP	
	RRLPPTP	
	RQLPPTP	
	RRLPRT	
	RPLPTRP	
	RPLPSRP	
	RILLPS	
	PPVPPRN	
	PSRASFGGASRPSPR	
	ETRPSPR	
	VTSPSPR	
	THLQSSRPSPR	
	NDSRPSPR	
	RPSRT	
	RPSRT	
	SASRPSPR	
	ATRPSPR	
	GRTPSHSRPSPR	
	PPASRPSPR	
	SRTVESC	
	SRTVESC	
	EPRTFYNYGHDSRPSPR	
	TRPSPR	
	RTTRPSPR	
	TTRPSPR	
	TTRPSPR	
	ITTRPSPR	
	TTRPSPR	
	PTTRPSPR	
	TTRPSPR	
	TTPRSTNLNL TSTTRPSPR	
	LTRPSPR	
	ITTRPSPR	
	Consensus	
	RPLPILP	
	RPLPMLP	
	RPLPMIP	
	RPLPSLP	
	RPLPSLP	
	RSLPPLP	
	RQLPIPP	
	RPLPLIP	
	RPLPPTP	
	RPQPPPP	
	RPLPPLP	
	SSCTEKT VSGVCGSRST	
	SSCMLPTDGVQCGSRSTP	
	SSCDGTQFLNCGSRSTN	
	SSCMQGAQLKCGSRST	
	SSCYREKDTVCGSRSTS	
	SSCLFEGAGTGGSRST	
	SSCDHTLGLGWCGSRST	
	SSCDTGRIAPGCGSRSTP	
	SSCGLDNAKTGGSRST	
	SSCSRAHETEMCGSRST	
	Consensus	
	RPLPILP	
	RPLPMLP	
	RPLPMIP	
	RPLPSLP	
	RPLPSLP	
	RSLPPLP	
	RQLPIPP	
	RPLPLIP	
	RPLPPTP	
	RPQPPPP	
	RPLPPLP	
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	SSCMLPTDGVQCGSRSTP	
	SSCDGTQFLNCGSRSTN	
	SSCMQGAQLKCGSRST	
	SSCYREKDTVCGSRSTS	
	SSCLFEGAGTGGSRST	
	SSCDHTLGLGWCGSRST	
	SSCDTGRIAPGCGSRSTP	
	SSCGLDNAKTGGSRST	
	SSCSRAHETEMCGSRST	
	Consensus	
	RPLPILP	
	RPLPMLP	
	RPLPMIP	
	RPLPSLP	
	RPLPSLP	
	RSLPPLP	
	RQLPIPP	
	RPLPLIP	
	RPLPPTP	
	RPQPPPP	
	RPLPPLP	
	SSCTEKT VSGVCGSRST	
	SSCMLPTDGVQCGSRSTP	
	SSCDGTQFLNCGSRSTN	
	SSCMQGAQLKCGSRST	
	SSCYREKDTVCGSRSTS	
	SSCLFEGAGTGGSRST	
	SSCDHTLGLGWCGSRST	
	SSCDTGRIAPGCGSRSTP	
	SSCGLDNAKTGGSRST	
	SSCSRAHETEMCGSRST	
	Consensus	
	RPLPILP	
	RPLPMLP	
	RPLPMIP	
	RPLPSLP	
	RPLPSLP	
	RSLPPLP	
	RQLPIPP	
	RPLPLIP	
	RPLPPTP	
	RPQPPPP	
	RPLPPLP	
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	SSCDGTQFLNCGSRSTN	
	SSCMQGAQLKCGSRST	
	SSCYREKDTVCGSRSTS	
	SSCLFEGAGTGGSRST	
	SSCDHTLGLGWCGSRST	
	SSCDTGRIAPGCGSRSTP	
	SSCGLDNAKTGGSRST	
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	RPLPPLP	
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	RPLPLIP	
	RPLPPTP	
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	RPLPPLP	
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	SSCMLPTDGVQCGSRSTP	
	SSCDGTQFLNCGSRSTN	
	SSCMQGAQLKCGSRST	
	SSCYREKDTVCGSRSTS	
	SSCLFEGAGTGGSRST	
	SSCDHTLGLGWCGSRST	
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	RPQPPPP	
	RPLPPLP	
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	RPLPMIP	
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	RPLPLIP	
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	RPQPPPP	
	RPLPPLP	
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	SSCDTGRIAPGCGSRSTP	
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	SSCSRAHETEMCGSRST	
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	RPQPPPP	
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	SSCDTGRIAPGCGSRSTP	
	SSCGLDNAKTGGSRST	
	SSCSRAHETEMCGSRST	
	Consensus	
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	RQLPIPP	
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	RPQPPPP	
	RPLPPLP	
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	SSCDHTLGLGWCGSRST	
	SSCDTGRIAPGCGSRSTP	
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	SSCSRAHETEMCGSRST	
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	RPLPMIP	
	RPLPSLP	
	RPLPSLP	
	RSLPPLP	
	RQLPIPP	
	RPLPLIP	
	RPLPPTP	
	RPQPPPP	
	RPLPPLP	
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	SSCMQGAQLKCGSRST	
	SSCYREKDTVCGSRSTS	
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	SSCDHTLGLGWCGSRST	
	SSCDTGRIAPGCGSRSTP	
	SSCGLDNAKTGGSRST	
	SSCSRAHETEMCGSRST	
	Consensus	
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	RPLPMLP	
	RPLPMIP	
	RPLPSLP	
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	RPQPPPP	
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	SSCGLDNAKTGGSRST	
	SSCSRAHETEMCGSRST	
	Consensus	
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	RPLPMLP	
	RPLPMIP	
	RPLPSLP	
	RPLPSLP	
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	RQLPIPP	
	RPLPLIP	
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	RPLPPLP	
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	SSCDTGRIAPGCGSRSTP	
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	SSCSRAHETEMCGSRST	
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	SSCDTGRIAPGCGSRSTP	
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	RPLPMLP	
	RPLPMIP	
	RPLPSLP	
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	RSLPPLP	
	RQLPIPP	
	RPLPLIP	
	RPLPPTP	
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	SSCDTGRIAPGCGSRSTP	
	SSCGLDNAKTGGSRST	
	SSCSRAHETEMCGSRST	
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	RPLPMLP	
	RPLPMIP	
	RPLPSLP	
	RPLPSLP	
	RSLPPLP	
	RQLPIPP	
	RPLPLIP	
	RPLPPTP	
	RPQPPPP	
	RPLPPLP	
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	SSCDTGRIAPGCGSRSTP	
	SSCGLDNAKTGGSRST	
	SSCSRAHETEMCGSRST	
	Consensus	
	RPLPILP	
	RPLPMLP	
	RPLPMIP	
	RPLPSLP	
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	RQLPIPP	
	RPLPLIP	
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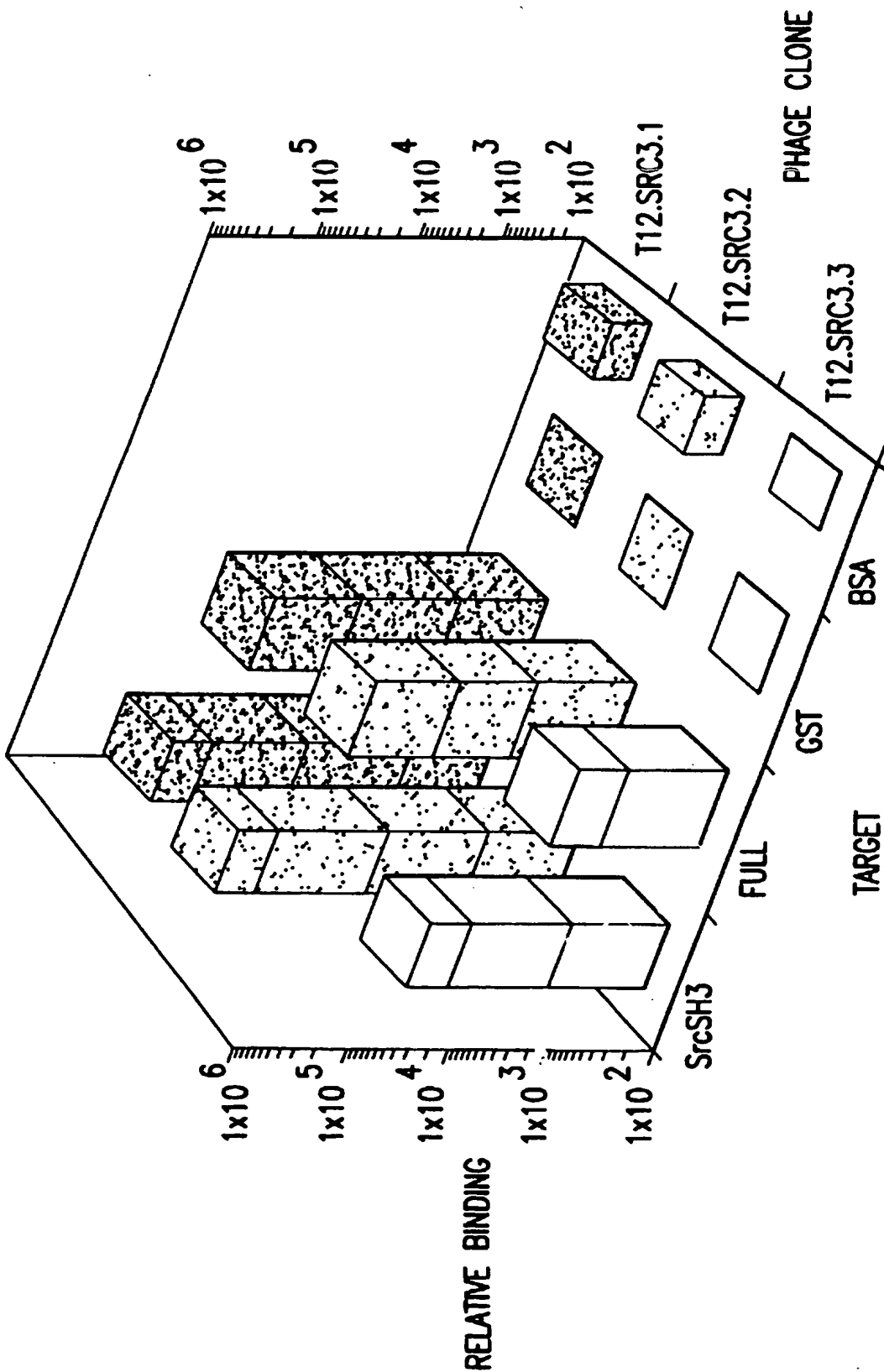


FIG.6

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OD ELISA VALUES

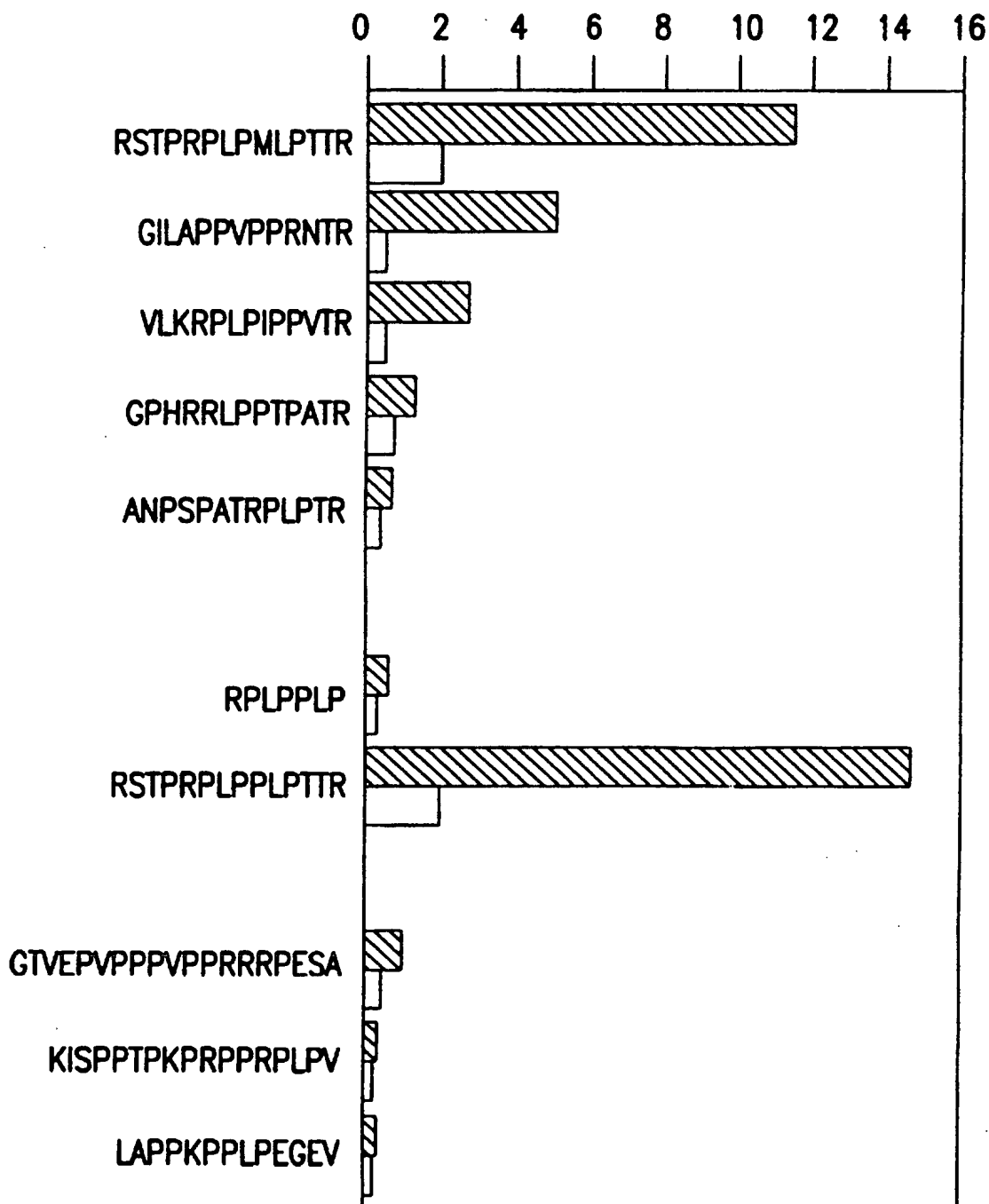


FIG.7

SUBSTITUTE SHEET (RULE 26)

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OD ELISA VALUES

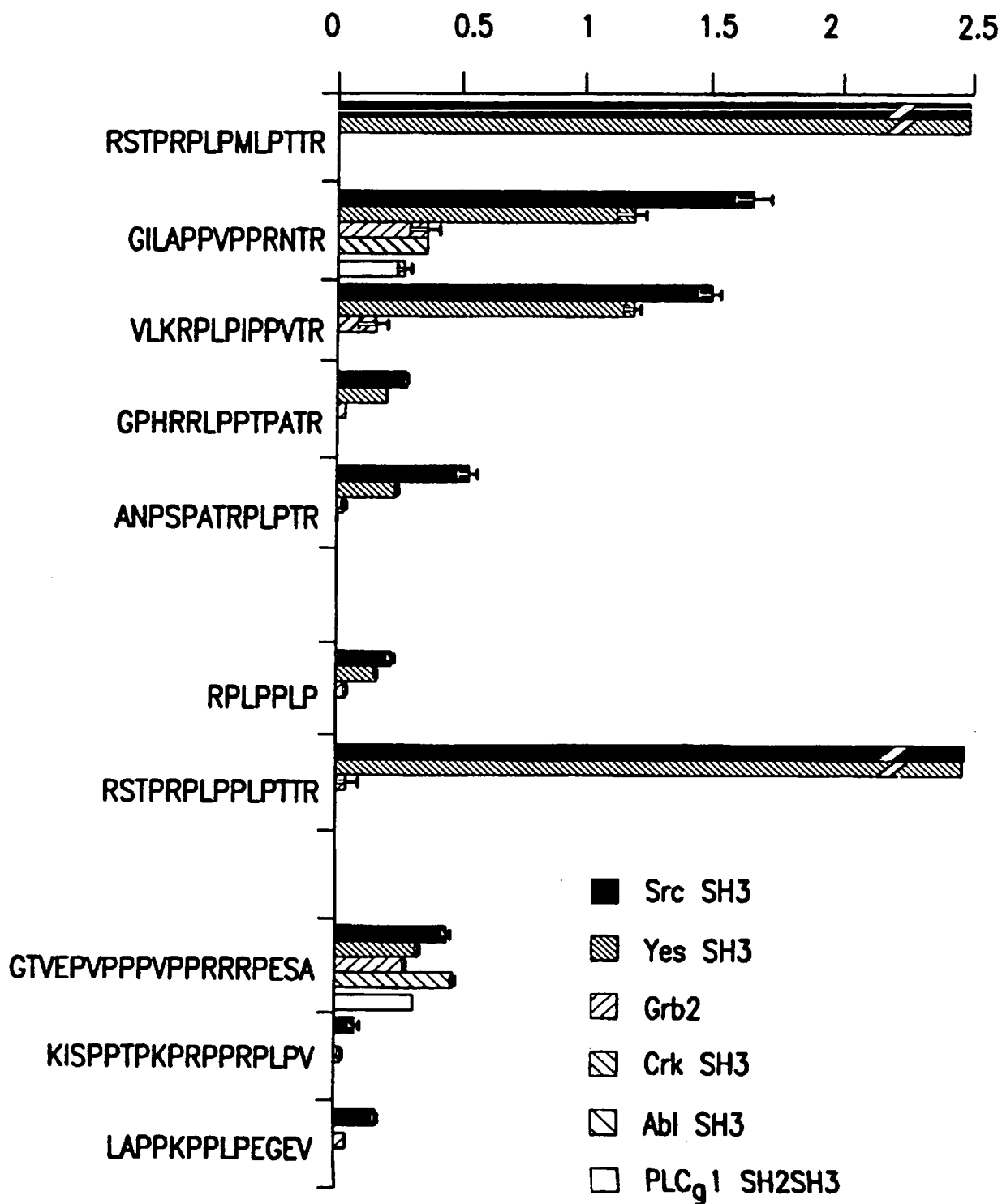


FIG.8

SUBSTITUTE SHEET (RULE 26)

PEPTIDES:
(MICROMOLAR
CONCENTRATION)

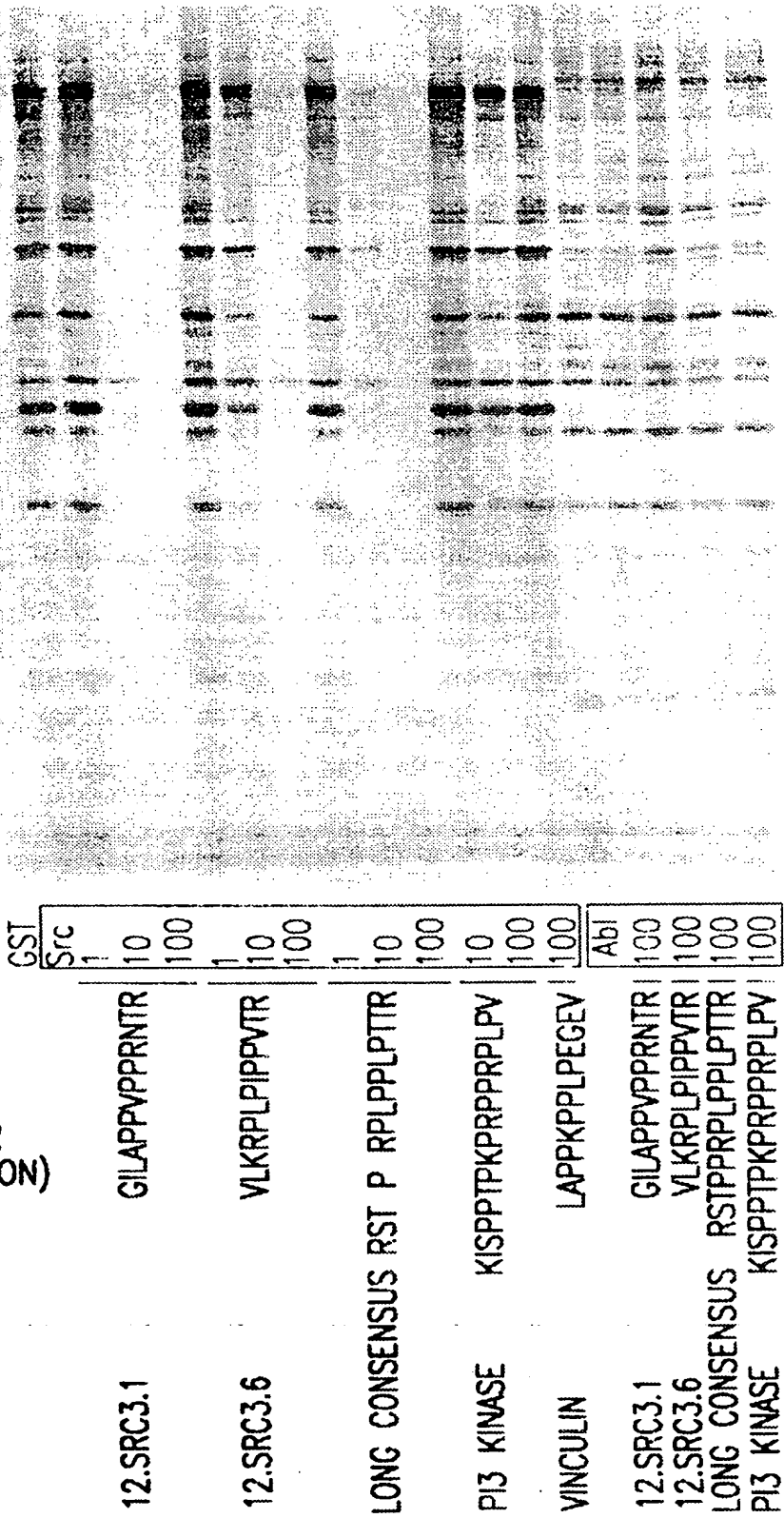


FIG.9

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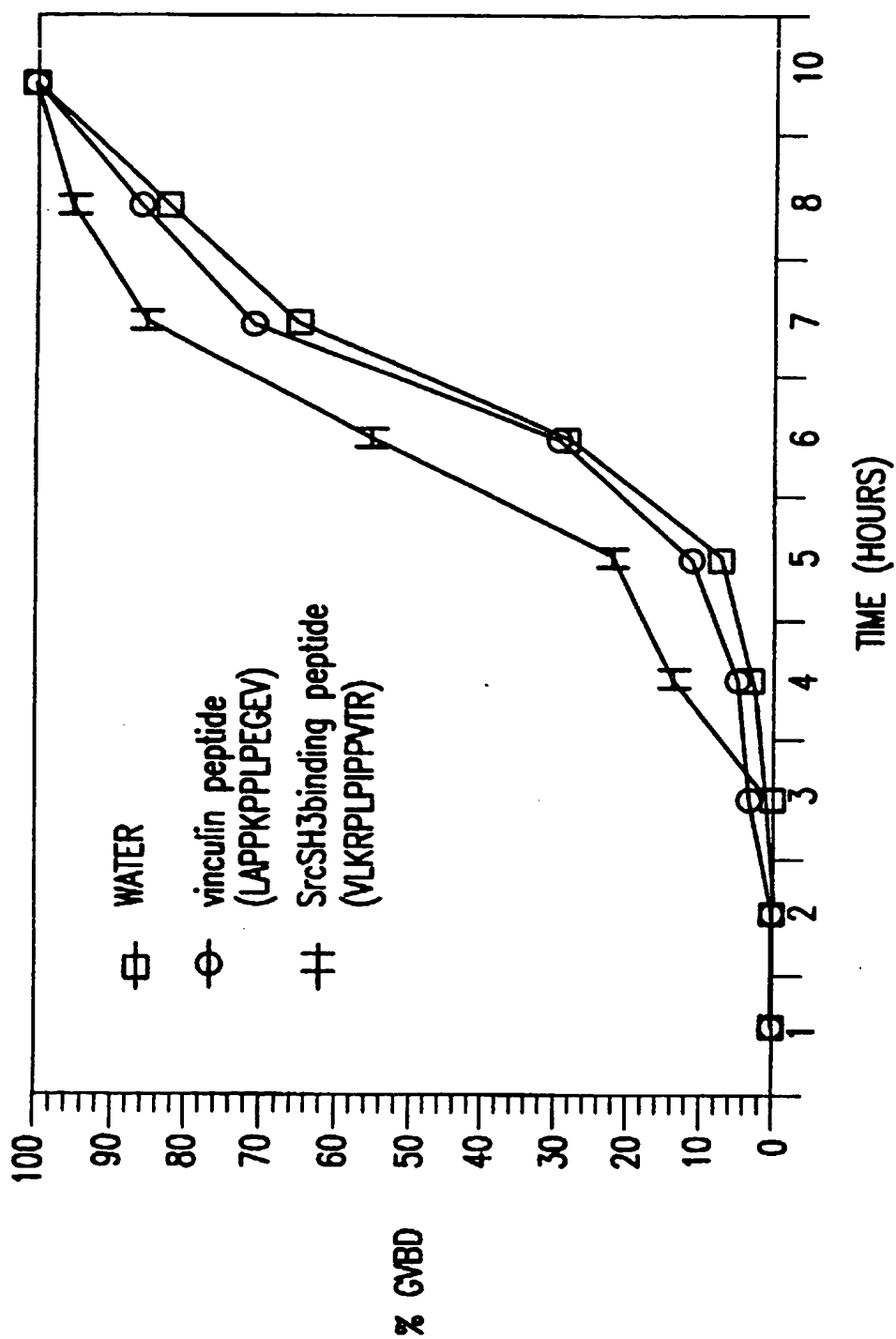


FIG.10

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FIG. 11A



FIG. 11B

SUBSTITUTE SHEET (RULE 26)

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FIG. 11C

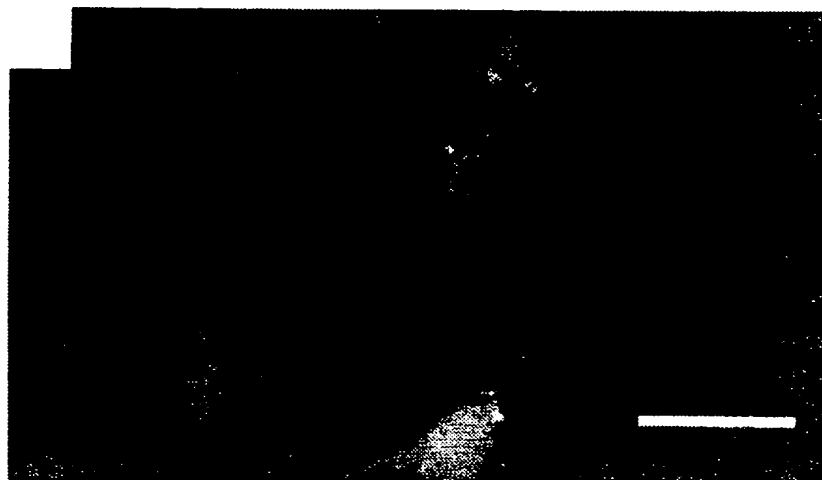


FIG. 11D

SUBSTITUTE SHEET (RULE 26)

ANNEAL OLIGONUCLEOTIDES

CTG TGC CTC GAG K NNK₆ CCA NNK₂ CCA NNK₆ TCT AGA CGT GTC AGT
AGA TCT GCA CAG TCA

FILL IN

CTG TGC CTC GAG K NNK₆ CCA NNK₂ CCA NNK₆ TCT AGA CGT GTC AGT
GAC ACG GAG CTC M NNM₆ GGT NNM₂ GGT NNM₆ AGA TCT GCA CAG TCA

CTG TGC C TC GAG K NNK₆ CCA NNK₂ CCA NNK₆ T CT AGA CGT GTC AGT
GAC ACG GAG CT C M NNM₆ GGT NNM₂ GGT NNM₆ AGA TC T GCA CAG TCA

DIGEST WITH
Xho I AND Xba I

TC GAG K NNK₆ CCA NNK₂ CCA NNK₆ T
C M NNM₆ GGT NNM₂ GGT NNM₆ AGA TC

GEL PURIFY
CUT
INSERT

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... TC GAG K NNK₆ CCA NNK₂ CCA NNK₆ TCT AGA. ...
... AG CTC M NNM₆ GGT NNM₂ GGT NNM₆ AGA CTC. ...

CLONE INTO
mBAX VECTOR

↑ S S/R X₆P X₂ P X₆ S R pIII

EXPRESS BPL

PEPTIDE CLEAVAGE
SITE

FIG.12

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mBAX

SIGNAL PEPTIDE
CLEAVAGE SITE

-1 ↓ +1

S S I D M P * T A S T M Y N M L H R N E P
 . . TCCTCGAGTATCGACATGCCCTTAGACTGCTAGCACTATGTACACATGCTTCATCGCAACGAGGCCA
 Xho I

. . . epitope, mAb . . .

G G R K L S P P A N D M P P A L L K R S R
 GGTGGAGGAAGTTGAGCCCGCCGCAACGACATGCCGCGCCCTCCTGAAGAGGTCCTAGA . .
 Xba I

FIG.13

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/09382

A. CLASSIFICATION OF SUBJECT MATTER IPC(6) : Please See Extra Sheet. US CL : 435/5, 7.1, 172.1, 320.1; 530/300; 514/2 According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 435/5, 7.1, 172.1, 320.1; 530/300; 514/2 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) APS, DIALOG, STN search terms: sh3, src, peptides		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P	The Journal of Biological Chemistry, Volume 269, Number 39, issued 30 Spetember 1994, Sparks et al., "Identification and Chracterization of Src SH3 Ligands from Phage-displayed Random Peptide Libraries", pages 23853-23856, see entire article.	1-74
X --- Y	Journal of the American Chemical Society, Volume 115, issued 1993, Chen et al. "Biased Combinatorial Libraries: Novel Ligands for the SH3 Domain of Phosphatidylinositol 3-Kinase", pages 12591-12592, see entire article, especially Tables I and II.	1-6, 24, 26, 28, 29, 53 ----- 7-23, 25, 27, 30-51, 53-74
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.		
* *A* *E* *L* *O* *P*	Special categories of cited documents: document defining the general state of the art which is not considered to be part of particular relevance earlier document published on or after the international filing date document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reasons (as specified) document referring to an oral disclosure, use, exhibition or other means document published prior to the international filing date but later than the priority date claimed	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art *G* document member of the same patent family
Date of the actual completion of the international search 19 OCTOBER 1995		Date of mailing of the international search report 01 NOV 1995
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230		Authorized officer <i>Lora M. Green</i> LORA M. GREEN Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/09382

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Science, Volume 249, issued 28 September 1990, Langer, "New Methods of Drug Discovery", pages 1527-1533, see entire article.	51, 52, 54-57
Y	Science, Volume 257, issued 07 August 1992, Cicchetti et al., "Identification of a Protein That Binds to the SH3 Region of Abl and Is Similar to BCR and GAP-rho"; pages 803-806, see entire article.	7-23, 25, 27, 30-50
Y	Gene, Volume 128, issued 1993, Kay et al., "An M13 Phage Library Displaying Random 38-amino-acid Peptides as a Source of Novel Sequences with Affinity to Selected Targets", pages 59-65, see entire article.	7-23, 25, 27, 30-48, 61-68

Form PCT/ISA/210 (continuation of second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US95/09382

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

G01N 33/53; C12Q 1/70; C12N 5/10. 7/01; C07K 7/00, 14/00; A61K 38/03

**CORRECTED
VERSION****CORRECTED
VERSION*****PCT**WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : G01N 33/53, C12Q 1/70, C12N 5/10, 7/01, C07K 7/00, 14/00, A61K 38/03		A1	(11) International Publication Number: WO 96/03649
			(43) International Publication Date: 8 February 1996 (08.02.96)
(21) International Application Number: PCT/US95/09382		(81) Designated States: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, IS, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TT, UA, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG), ARIPO patent (KE, MW, SD, SZ, UG).	
(22) International Filing Date: 24 July 1995 (24.07.95)		Published <i>With international search report.</i>	
(30) Priority Data: 278,865 22 July 1994 (22.07.94) US 483,555 7 June 1995 (07.06.95) US			
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(74) Agents: MISROCK, S., Leslie et al.; Pennie & Edmonds, 1155 Avenue of the Americas, New York, NY 10036 (US).			
(54) Title: Src SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME			
(57) Abstract <p>Peptides having general and specific binding affinities for the Src homology region 3 (SH3) domains of proteins are disclosed in the present invention. In particular, SH3 binding peptides have been isolated from three phage-displayed random peptide libraries which had been screened for isolates that bind to bacterial fusion proteins comprising SH3 and glutathione S-transferase (GST). Preferred peptides are disclosed which comprise a core 7-mer sequence (preferably, a consensus motif) and two or more, preferably at least six, additional amino acid residues flanking the core sequence, for a total length of 9, preferably at least 13, amino acid residues and no more than about 45 amino acid residues. Such peptides manifest preferential binding affinities for certain SH3 domains. The preferred peptides exhibit specific binding affinities for the Src-family of proteins. <i>In vitro</i> and <i>in vivo</i> results are presented which demonstrate the biochemical activity of such peptides.</p>			

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**Src SH3 BINDING PEPTIDES AND
METHODS OF ISOLATING AND USING SAME**

1. Field of the Invention

5 The present invention relates to SH3 binding peptides having a broad range of binding specificities. That is, certain members of the SH3 binding peptides disclosed bind with approximately the same facility with SH3 domains derived from different SH3 domain-containing proteins. Other members, in contrast, bind with a much greater degree of affinity for specific SH3 domains. The SH3 binding peptides are obtained from random peptide libraries that are also phage-displayed. Methods are described of obtaining the phage clones that bind to the SH3 domain targets and of
10 determining their relevant nucleotide sequences and consequent primary amino acid sequence of the binding peptides. The resulting SH3 binding proteins are useful in a number of ways, including, but not limited to, providing a method of modulating signal transduction pathways at the
15 cellular level, of modulating oncogenic protein activity or of providing lead compounds for development of drugs with the ability to modulate broad classes, as well as specific classes, of proteins involved in signal transduction.

2. Background of the Invention

2.1. Src and the SH3 Domain

 Among a number of proteins involved in eukaryotic cell signaling, there is a common sequence motif called the SH3 domain. It is 50-70 amino acids in length,
30 moderately conserved in primary structure, and can be present from one to several times in a large number of proteins involved in signal transduction and in cytoskeletal proteins.

 The protein pp60c-src represents a family of at least nine non-receptor protein tyrosine kinases (NR-PTKs).
35 Members of this family share an overall structural organization comprising a series of catalytic and non-catalytic domains. In Src, a 14-amino-acid myristylation

signal resides at the extreme amino-terminus, and is followed by a unique region that is not highly conserved among family members. Following this region are two highly conserved 60- and 100-amino-acid regions, the Src homology (SH) domains 3 and 2, respectively. SH2 and SH3 domains have been shown to play an important role in mediating protein-protein interactions in a variety of signaling pathways. Koch, C.A., et al., in Science (1991) 252:668-74. The carboxy-terminal half of Src contains the PTK catalytic domain, as well as a negative regulatory tyrosine (Y527) near the carboxy terminus. Phosphorylation of this residue (e.g., by Csk) results in the inhibition of PTK activity. Cooper, J.A., et al., in Science (1986) 231:1431-1434. Mutation of Y527->F generates forms of Src with increased PTK and oncogenic activity. Cartwright, C.A., et al., in Cell (1987) 49:83-91; Kmiecik, T.E., et al., in Cell (1987) 49:65-73; and Piwnicka-Worms, H., et al., in Cell (1987) 75-82.

The fact that some mutations which result in increased Src PTK and transforming activity map to the Src SH2 (Seidel-Dugan, C., et al., in Mol. Cell. Biol. (1992) 12:1835-45; and Hirai, H. and Varmus, H.E. in Mol. Cell. Biol. (1990) 10:1307-1318) and SH3 domains (Seidel-Dugan, C., et al., supra; Hirai, H. and Varmus, H.E., supra; Superti-Furga, G., et al., in Embo. J. (1993) 12:2625-34; and Potts, W.M., et al., in Oncogene Res. (1988) 3:343-355) suggests a negative regulatory role for these domains. That phosphotyrosine residues within specific sequence contexts represent high affinity ligands for SH2 domains suggests a model in which the SH2 domain participates in Y527-mediated inhibition of PTK activity by binding phosphorylated Y527, thereby locking the kinase domain in an inactive configuration. Matsuda, M., Mayer, B.J., et al., in Science (1990) 248:1537-1539. This model is supported by the observation that phosphopeptides corresponding to the carboxy-terminal tail of Src bind active, but not inactive, variants of Src. Russell, R.R., et al., in Proc. Natl. Acad. Sci. U S A (1991) 88:10696-700; and Liu, X., et al., in Oncogene (1993) 8:1119-1126.

The mechanism of SH3-mediated inhibition of Src PTK activity remains unclear. There is evidence that pY527-mediated inhibition of Src PTK activity involves the SH3 domain as well as the SH2 domain. Okada, M., Howell, et al., in J. Biol. Chem. (1993) 268:18070-5; Murphy, S.M., et al., in Mol. Cell. Biol. (1993) 13:5290-300; and Superti-Furga, G., et al., *supra*. Although these effects are thought to be a consequence of SH3-mediated protein-protein interactions, precisely how the Src SH3 domain exerts its negative regulatory effect is unclear. Identification of high affinity ligands for the Src SH3 domain could help resolve these issues.

2.2. Protein Tyrosine Kinases and The Immune Response

Src-related tyrosine kinases are expressed in a variety of cell types including those of the immune system (lymphocytes, T cells, B cells, and natural killer cells) and the central nervous system (neural cells, neurons, oligodendrocytes, parts of the cerebellum, and the like). Umemori, H. et al., in Brain Res. Mol. Brain Res. (1992) Dec. 16(3-4):303-310. Their presence in these cells and tissues and their interaction with specific cell surface receptors and immunomodulatory proteins (such as T cell antigen receptor, CD14, CD2, CD4, CD40 or CD45) suggest that these kinases serve an important role in the signalling pathways of not only the central nervous system but of the immune system, as well. See, e.g., Ren, C.L. et al., in J. Exp. Med. (1994) 179(2):673-680 (signal transduction via CD40 involves activation of Lyn kinase); Donovan, J.A. and Koretzky, G.A., in J. Am. Soc. Nephrol. (1993) 4(4):976-985 (CD45, the immune response, and regulation of Lck and Fyn kinases); and Carmo, A.M. et al., in Eur. J. Immunol. (1993) 23(9):2196-2201 (physical association of the cytoplasmic domain of CD2 with p56lck and p59fyn). For instance, mice with disruptions in their Src-like genes, Hck and Fgr, possess macrophages with impaired phagocytic activity or exhibit a novel immunodeficiency

characterized by an increased susceptibility to infection with *Listeria monocytogenes*. Lowell, C.A. et al., in Genes Dev. (1994) 8(4):387-398. Also, it has been shown that bacterial lipopolysaccharide (LPS) activates CD14-associated p56lyn, p68hck, and p59c-fgr, while inducing the production of lymphokines, such as TNF-alpha, IL-1, IL-6, and IL-8. Inhibition of the protein tyrosine kinases blocks production of TNF-alpha and IL-1.

10 2.3. SH3 Binding Peptides

As mentioned above, it has long been suspected that SH3 domains are sites of protein-protein interaction, but it has been unclear what SH3 domains actually bind. Efforts to identify ligands for SH3 domains have led to the
15 characterization of a number of SH3-binding proteins, including 3BP1 and 2 (Ren, R., Mayer, et al., in Science (1993) 259:1157-61), SOS (Olivier, J.P., et al., in Cell (1993) 73:179-91; and Rozakis-Adcock, M., et al., in Nature (1993) 363:83-5), p85 PI-3' Kinase (Xingquan, L., et al., in
20 Mol. Cell. Biol. (1993) 13:5225-5232), dynamin (Gout, I., et al., in Cell (1993) 75:25-36), AFAP-110 (Flynn, D.C., et al., in Mol. Cell. Biol. (1993) 13:7892-7900), and CD42 (Barford, E.T., et al., in J. Biol. Chem. (1993) 268:26059-26062). These proteins tend to possess short, proline-rich stretches
25 of amino acids, some of which have been directly implicated in SH3 binding. A variety of consensus sequences have been proposed, although the similarity among proline-rich regions of different SH3-binding proteins tends to be fairly low. Also, attempts to build consensus sequences are likely
30 complicated by the incorporation of data from proteins that bind different SH3 domains.

Thus, Cicchetti, P., et al., in Science (1992) 257:803-806, published their work relating to the isolation and sequencing of two naturally-occurring proteins that could be
35 bound *in vitro* by the SH3 domain of the *abl* oncogene product. These workers found that SH3 domains bind short, proline-rich regions of such proteins. Subsequently, this same group

disclosed further results (Ren, R. et al., supra) in which the SH3 binding sites of the SH3 binding proteins were localized to "a nine- or ten-amino acid stretch rich in proline residues." A consensus sequence incorporating the features of the SH3 binding sites of four SH3 binding proteins was proposed: XPXXPPPWX (SEQ ID NO:1), wherein X indicates a position in the amino acid sequence which is not conserved among the four SH3 binding proteins, P represents proline, and W indicates a hydrophobic amino acid residue, such as P or L.

The screening of complex random peptide libraries has been used to identify peptide epitopes for monoclonal (Scott, J.K. and Smith, G.P. in Science (1990) 249:386-390) and polyclonal (Kay, B.K., et al., in Gene (1993) 128:59-65) antibodies, as well as peptide ligands for a variety of proteins, including streptavidin (Devlin, J.J., et al., in Science (1990) 249:404-406; and Lam, K., et al., in Nature (1991) 354:82-84), the endoplasmic reticulum chaperone BiP (Blond-Elguindi, S., et al., in Cell (1993) 75:717-728), and CaM (Dedman, J.R., et al., in J. Biol. Chem. (1993) 268:23025-23030).

Recently, Chen, J.K. et al., in J. Am. Chem. Soc. (1993) 115:12591-12592, described ligands for the SH3 domain of phosphatidylinositol 3-kinase (PI-3' Kinase) which were isolated from a biased combinatorial library. A "biased" library is to be distinguished from a "random" library in that the amino acid residue at certain positions of the synthetic peptide are fixed, i.e., not allowed to vary in a random fashion. Indeed, as stated by these research workers, screening of a "random" combinatorial library failed to yield suitable ligands for a PI-3' Kinase SH3 domain probe. The binding affinities of these unsuitable ligands was described as weak, >100 μ M, based on dissociation constants measured by the Biosensor System (BIAcore).

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More recently, Yu, et al. (Yu, H., et al., in Cell (1994) 76:933-945) used a "biased" synthetic peptide library

of the form XXXPPXPXX (SEQ ID NO:2), wherein X represents any amino acid other than cysteine, to identify a series of peptides which bind the Src and PI-3' Kinase SH3 domains. The bias was accomplished by fixing the proline residues at the specific amino acid positions indicated for the "random" peptide. As stated previously, without this bias, the technique disclosed fails to identify any SH3 domain-binding peptides.

A consensus sequence, based on 13 binding peptides was suggested: RXLPPrPXX (SEQ ID NO:3), where X tends to be a basic residue (like R, K or H). The binding affinities of several SH3 binding peptides were disclosed as ranging from 8.7 to 30 μ M. A "composite" peptide, RKLPPRR (SEQ ID NO:4), was reported to have a binding affinity of 7.6 μ M. This value compares favorably to the binding affinity of the peptide, VPPPVPPRR (SEQ ID NO:5), to the N-terminal SH3 domain of Grb2. See, Kraulis, P.J. J. Appl. Crystallogr. (1991) 24:946. Recognizing the limitations of their technique, Chen and co-workers, *supra*, stated that their results "illustrate the utility of biased combinatorial libraries for ligand discovery in systems where there is some general knowledge of the ligand-binding characteristics of the receptor" (emphasis added).

Yu and co-workers, *supra*, further described an SH3 binding site consensus sequence, Xp \emptyset PpXP (SEQ ID NO:6), wherein X represents non-conserved residues, \emptyset represents hydrophobic residues, P is proline, and p represents residues that tend to be proline. A consensus motif of RXLPPrPXX (SEQ ID NO:7), where X represents any amino acid other than cysteine, was proposed for ligands of PI-3' Kinase SH3 domain. A consensus motif of RXLPPLP \emptyset (SEQ ID NO:8), where \emptyset represents hydrophobic residues, was proposed for ligands of Src SH3 domain. Still, the dissociation constants reported for the 9-mer peptides ranged only from about 8-70 μ M and selectivity between one type of SH3 domain and another was relatively poor, the K_D s differing by only about a factor of four.

Hence, there remains a need to develop techniques for the identification of Src SH3 binding peptides which do not rely on such "biased" combinatorial peptide libraries that are limited to a partially predetermined set of amino acid sequences. Indeed, the isolation of SH3 binding peptides from a "random" peptide library has not been achieved successfully before now. Furthermore, particular peptides having much greater binding affinities, whether general or more selective binding for specific SH3 domains, remain to be identified. Binding peptides specific for particular SH3 domains are useful, for example, in modulating the activity of a particular SH3 domain-containing protein, while leaving others bearing an SH3 domain unaffected. Still, the more promiscuous general binding peptides are useful for the modulation of a broad spectrum of SH3 domain-containing proteins.

The present invention relates to such SH3 binding peptides, methods for their identification, and compositions comprising same. In particular, peptides comprising particular sequences of amino acid residues are disclosed which were isolated from random peptide libraries. In the present invention, clones were isolated from a phage-displayed random peptide library which exhibited strong binding affinities for SH3 domain-containing protein targets. Some of these protein targets, include Abl, Src, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, and p85 PI-3' Kinase. From the nucleotide sequence of the binding phage, the amino acid sequence of the peptide inserts has been deduced. Synthetic peptides having the desired amino acid sequences are shown to bind the SH3 domain of the target proteins. In particular, synthetic peptides combining a core consensus sequence and additional amino acid residues flanking the core sequence are especially effective at binding to particular target protein SH3 domains. The SH3 binding peptides disclosed herein can be utilized in a number of ways, including the potential modulation of oncogenic protein activity in vivo. These peptides also serve as useful aids in the production of

peptidomimetic drugs that modulate a large class of proteins involved in signal transduction pathways and oncogenesis.

3. Summary of the Invention

Accordingly, three phage-displayed random peptide libraries were screened for isolates that bind to bacterial fusion proteins consisting of the Src homology region 3 (SH3) and glutathione S-transferase (GST). DNA sequencing of the isolates showed that they contained sequences that resemble the consensus motif, RPLPPLP (SEQ ID NO:9), within their 8, 22, or 36 amino acid long random regions. When peptides were synthesized corresponding to the pIII inserts of the SH3-binding phage, they bound to the GST fusions of the SH3 domains of Src and the Src-related proteins, such as Yes, but not of Grb2, Crk, Abl, or PLC γ 1. The synthesized peptides bind quite well to the Src SH3 domain and act as potent competitors of natural Src SH3 interactions in cell lysates. For instance, these peptides can compete with radiolabelled proteins from cell lysates in binding to immobilized Src-GST, with an apparent IC₅₀ of 1-10 μ M. When a peptide, bearing the consensus sequence RPLPPLP (SEQ ID NO:9) was injected into *Xenopus laevis* oocytes, it accelerated the rate of progesterone-induced maturation. These results demonstrate the utility of phage-displayed random peptide libraries in identifying SH3-binding peptide sequences and that such identified peptides exhibit both *in vivo* and *in vitro* biological activity.

Thus, it is an object of the present invention to provide peptides having at least nine and up to forty-five amino acid residues, including an amino acid sequence of the formula, R-2-L-P-5-6-P-8-9 (SEQ ID NO:10), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 2 represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, 8 represents any amino acid residue except cysteine, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard

one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src, provided that said peptide is not R-P-L-P-P-L-P-T-S (SEQ ID NO:11). In a particular embodiment of the present invention, the peptides also exhibit a binding affinity for the SH3 domain of Src-related proteins, including Yes, Fyn, Lyn, Lck, Hck and Fgr.

The present invention also contemplates SH3 domain-binding peptides that further comprise a C-terminal-flanking amino acid sequence of the formula 10, 10-11, 10-11-12, 10-11-12-13 (SEQ ID NO:12) or 10-11-12-13-14 (SEQ ID NO:13), in which each number represents any amino acid residue except cysteine, such that 10 is bound to 9 by a peptide bond. Furthermore, peptides are also provided which further comprise an N-terminal-flanking amino acid sequence of the formula 1', 2'-1', 3'-2'-1' or 4'-3'-2'-1' (SEQ ID NO:14) in which each number represents any amino acid residue except cysteine, such that 1' is bound to R by a peptide bond.

Thus, in a particular embodiment, a peptide is disclosed having at least thirteen and up to forty-five amino acid residues, including an amino acid sequence of the formula, 3'-2'-1'-R-2-L-P-5-6-P-8-9-10 (SEQ ID NO:15), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 3', 2', 1', 2, 8, and 10 each represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src.

The present invention also seeks to provide new consensus sequences or motifs that reflect variations in SH3 domain binding selectivities or specificities. The present invention also contemplates conjugates of the SH3 binding peptides and a second molecule or chemical moiety. This second molecule may be any desired substance whose delivery to the region of the SH3 domain of a particular protein (or

cells containing the protein) is sought. Possible target cells include, but are not limited to, neural cells, immune cells (e.g., T cells, B cells, natural killer cells, and the like), osteoclasts, platelets, epidermal cells, and the like, which cells express Src, Src-related proteins, and potentially, other SH3 domain-containing proteins. In this manner, the modulation of the biological activity of proteins bearing an SH3 domain can be accomplished.

Other methods and compositions consistent with the objectives of the present invention are likewise disclosed. In particular, a method is disclosed of modulating the activity of Src or Src-related proteins comprising administering a composition comprising an effective amount of a peptide of the present invention and a carrier, preferably a pharmaceutically acceptable carrier. In a specific embodiment, the contemplated method results in the inhibition of the activity of Src or Src-related proteins. Alternatively, the method is effective to activate Src or Src-related proteins.

In yet another embodiment, a method is disclosed of identifying a peptide having a region that binds to an SH3 domain comprising: (a) providing an immobilized target protein comprising an SH3 domain; (b) incubating the immobilized target protein with an aliquot taken from a random peptide library; (c) washing unbound library peptides from the immobilized target protein; (d) recovering the peptide bound to the immobilized target protein; and (e) determining the primary sequence of the SH3 domain-binding peptide.

Moreover, a method is disclosed of imaging cells, tissues, and organs in which Src or Src-related proteins are expressed, which comprises administering an effective amount of a composition comprising an SH3 domain-binding peptide conjugated to detectable label or an imaging agent.

Other objectives of the present invention will become apparent to one of ordinary skill in the art after

consideration of the above disclosure and the following detailed description of the preferred embodiments.

4. Brief Description of the Figures

5 FIG. 1 illustrates a scheme for the generation of a random 36 amino acid peptide library (TSAR-9; e.g., SEQ ID NO:16). Oligonucleotides were synthesized (SEQ ID NOS:17-18), converted into double-stranded DNA, cleaved with restriction enzymes (SEQ ID NOS:19-20), and cloned into the
10 M13 vector, m663. The random peptide region encoded by the oligonucleotides is shown in the box (SEQ ID NO:16) and is situated at the N-terminus of mature protein III (SEQ ID NO:21).

 FIG. 2 illustrates a scheme for the generation of a
15 random 22 amino acid peptide library (TSAR-12; e.g., SEQ ID NO:23). Oligonucleotides were synthesized (SEQ ID NOS:24-25), converted into double-stranded DNA, cleaved with restriction enzymes (SEQ ID NOS:26-27), and cloned into the M13 vector, m663. The random peptide region encoded by the
20 oligonucleotides is shown in the box (SEQ ID NO:23) and is situated at the N-terminus of mature protein III (SEQ ID NO:28).

 FIG. 3 illustrates a scheme for the generation of a random 8 amino acid peptide library (R8C; SEQ ID NO:30).
25 Oligonucleotides were synthesized (SEQ ID NOS:31-32), converted into double-stranded DNA, cleaved with restriction enzymes (SEQ ID NOS:33-34), and cloned into the M13 vector, m663. The random peptide region (SEQ ID NO:30) is flanked by cysteine residues and is situated at the N-terminus of mature
30 protein III (SEQ ID NO:35).

 FIG. 4 illustrates the possible origin of one class of double-insert R8C recombinants (e.g., encoding SEQ ID NO:36). Double-stranded oligonucleotides (e.g., SEQ ID NO:37) may have ligated in a head-to-head fashion at the Xba I site
35 prior to cloning in the Xho I- Xba I cleaved M13 vector.

 FIG. 5 shows a list of random peptide recombinants (SEQ ID NOS:38-61 and 106) isolated by the method of the present

inv nti n and the display d peptid s qu nce. The amin acid sequences ar aligned to highlight the core sequenc s. The flanking sequences ar shown to the N-terminal and C-t rmin al ends of the core sequence.

5 FIG. 6 graphically illustrates the relative binding affinities of selected phage clones for various SH3 domains. The results indicate that certain amino acid sequences provide generic SH3 domain binding, while others can provide greater selectivity for the SH3 domain of Src. Still other
10 clones exhibit Src SH3 domain preferential binding.

FIG. 7 shows the binding of synthetic peptides (SEQ ID NOS:9 and 62-70) representing Src SH3-selected phage inserts to Src SH3-GST fusion target (shaded columns) over background GST binding (unshaded columns) relative to the core peptide
15 RPLPPLP (SEQ ID NO:9) and proline-rich peptide segments derived from naturally occurring proteins. Bound biotinylated peptide was detected with streptavidin-alkaline phosphatase ELISA. Each point was performed in triplicate; average absorbance at 405 nm is presented. Error bars
20 represent SD.

FIG. 8 illustrates the relative specificity of selected peptides (SEQ ID NOS:9 and 62-70) for SH3 domains derived from different proteins. In particular, the binding affinities of the peptides for the SH3 domains of the
25 following protein fusion targets were tested: Src SH3-GST, Yes SH3-GST, Grb2-GST, Crk SH3-GST, Abl SH3-GST, PLC γ 1 SH2SH3-GST. Bound biotinylated peptide was detected with streptavidin-alkaline phosphatase. Each point was performed in triplicate; values are average signal (absorbance at 405
30 nm) above GST background, with error bars representing standard deviation. Hatched bars indicate saturation of the ELISA signal.

FIG. 9 presents the results of competition experiments in which selected peptides were found to inhibit the binding
35 of pr t ins from cell lysates to immobilized Src SH3-GST r Abl SH3-GST protein fusion targets.

FIG. 10 presents a graph illustrating the increase in rate of progesterone-induced maturation of oocytes injected with an SH3 domain-binding peptide, VLKRPLPIPPVTR (SEQ ID NO:64), of the present invention. Briefly, Stage VI oocytes were prepared and injected as previously described (see, Kay, B.K., in Methods in Cell Biol. (1991) 36:663-669). Oocytes were injected with 40 nL of 100 μ M test peptide or water. After injection, the oocytes were placed in 2 μ g/mL progesterone (Sigma, St. Louis, MO) and scored hourly for germinal vesicle breakdown (GVBD).

FIG. 11 shows the results of fluorescence experiments in which certain peptides, Panel A = VLKRPLPIPPVTR (SEQ ID NO:64), Panel B = GILAPPVPPRNTR (SEQ ID NO:63), Panel C = RSTPRPLPLPTTR (SEQ ID NO:67), of the invention were shown to localize within cellular compartments thought to contain Src or Src-related proteins.

FIG. 12 illustrates a scheme for the generation of a biased peptide library. Oligonucleotides were synthesized, converted into double-stranded DNA, cleaved with restriction enzymes XhoI and XbaI, and cloned into the mBAX vector, described further below in the Examples section. The biased peptide region is situated at the N-terminus of mature pIII protein.

FIG. 13 illustrates the peptide sequence encoded in the mBAX vector situated at the N-terminus of mature pIII protein.

5. Detailed Description of the Preferred Embodiments

5.1. General Considerations

The present invention relates to peptides that exhibit a binding affinity for an SH3 domain, which domain has been found to be present in a number of physiologically significant proteins. In particular, peptides are disclosed which exhibit general binding characteristics to the SH3 domains found in a group of proteins, including but not limited to Abl, Src, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, and p85 PI-3' Kinase. Preferred peptides exhibit selective, if

not specific, binding affinity for the SH3 domain of Src. As described herein, the peptides of the present invention include a core sequence, preferably a consensus sequence, and additional amino acid residues that flank the core sequence.

5 These peptides, including the methods for their identification, are described in greater detail, below.

Thus, in a specific embodiment of the invention, peptides are provided which have at least nine and up to about forty-five amino acid residues, including an amino acid
10 sequence resembling the formula,

R-2-L-P-5-6-P-8-9 (SEQ ID NO:10),

positioned anywhere along the peptide. In the above-mentioned formula, each number represents an amino acid residue, such that 2 represents any amino acid residue except
15 cysteine, 5 and 6 each represents a hydrophobic amino acid residue, 8 represents any amino acid residue except cysteine, and 9 represents a hydrophilic amino acid residue except cysteine. Each letter used in the formulas herein represent the standard one-letter symbol for the corresponding amino
20 acid. When the peptide is a 9-mer, the peptide

R-P-L-P-P-L-P-T-S (SEQ ID NO:11) is excluded. The peptides of particular interest are those that exhibit a binding affinity for the SH3 domain of Src and Src-related proteins, including Yes, Fyn, Lyn, Lck, Hck and Fgr. Preferably, the
25 peptides of the invention exhibit a binding affinity for the SH3 domain of Src, which is at least three-fold, more preferably at least four-fold, most preferably at least about five-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9). In still other embodiments, the peptides
30 exhibit a binding affinity for the SH3 domain of Src which is at least ten-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9).

In specific embodiments, peptides are disclosed in which the various amino acid residues at the indicated positions
35 may independently have the following preferred identities: 2 is a P, R, A, L, Q, E or S, more preferably P or R; 5 represents a P, M, I or L, more preferably P or M; 6 is a P,

L, I or V, more preferably P or L; 8 is a T, R, P, I, N, E, V, S, A, G or L, more preferably T or R; and 9 is a T, R, S, H or D, more preferably T or R. Despite the preference for hydrophobic amino acid residues at 5 and 6, in some cases it may be desirable to have hydrophilic amino acid residues at these positions. Specifically, amino acid residue 5 may be a T, R or S, and amino acid residue 6 may be a T or R. Likewise, while a hydrophilic amino acid residue is preferred at position 9, in some instances a hydrophobic residue, such as a P or A, may be desirable.

The present invention also contemplates SH3 domain-binding peptides with a minimum length of 10, 11, 12, 13, 14, 15 or more amino acids. Such peptides contain additional amino acid residues flanking the core sequence of R-2-L-P-5-6-P (SEQ ID NO:71) either at the C-terminal end, the N-terminal end or both. Thus, for example, such peptides include those that further comprise a C-terminal-flanking amino acid sequence of the formula 10, 10-11, 10-11-12, 10-11-12-13 (SEQ ID NO:12) or 10-11-12-13-14 (SEQ ID NO:13), in which each number represents any amino acid residue except cysteine, such that the amino acid residue 10 is bound to the amino acid residue 9 by a peptide bond. In that case, specific embodiments include an amino acid residue 10 which is T, R, L, S, D, P, A or N, preferably T or R, an amino acid residue 11 which is R, P, A, Q, S or T, preferably R or P, an amino acid residue 12 which is P, S, R or T, preferably P or S, an amino acid residue 13 which is P, S, R, F, H or T, preferably P or S, and an amino acid residue 14 which is S, R, G or T, preferably, S or R.

Furthermore, peptides are also provided which further comprise an N-terminal-flanking amino acid sequence of the formula 1', 2'-1', 3'-2'-1' or 4'-3'-2'-1' (SEQ ID NO:14) in which each number represents any amino acid residue except cysteine, such that 1' is bound to R by a peptide bond. In such a case, specific embodiments are provided in which the amino acid residue 1' is T, P, S, N, F, W, K, H, Q or G, preferably T or P, wherein the amino acid residue 2' is S, T,

G, P, R, Q, L, A or H, preferably S or T, where in the amino acid residue 3' is R, S, P, G, A, V, Y or L, preferably S or T, and wherein the amino acid residue 4' is R, S, V, T, G, L or F, preferably R or S.

5 In a particular embodiment, a peptide is disclosed having at least thirteen and up to forty-five amino acid residues, including an amino acid sequence of the formula, 3'-2'-1'-R-2-L-P-5-6-P-8-9-10 (SEQ ID NO:15), positioned
10 anywhere along the peptide, in which each number represents an amino acid residue, such that 3', 2', 1', 2, 8, and 10 each represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the
15 corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src. Preferred 13-mers include, but are not limited to, those having an amino acid residue 5 which is a P or M, an amino acid residue 1' which is T, P, S or N, an amino acid residue 2' which is S or T, an
20 amino acid residue 3' which is R or S, and an amino acid residue 10 which is T or R. In all the SH3 domain-binding peptides described herein, the prohibition against the use of the hydrophilic amino acid residue cysteine (C) does not extend beyond the 7-mer "core" sequence and the additional
25 amino acid residues flanking the core up to a total (core + flanking) of about 20 amino acids. That is, the occasional use of a cysteine is not absolutely prohibited. What should be kept in mind is that the potential for the formation of intramolecular disulfide bonds, to form a cyclic structure,
30 be minimized as much as possible. Applicants have found that cyclized structures appear to be disfavored, at least with potential binding peptides of less than about 15 amino acid residues in length. The concern for the formation of cyclized structures comprising the core sequence diminishes
35 with increasing size of the peptide. Presumably, a large enough structure, though cyclic, may allow the critical core sequence to adopt a more or less linear conformation.

In particular, specific peptides are disclosed which exhibit binding affinities to SH3 domains. These include the peptides, RSTPRPLPMLPTTR (SEQ ID NO. 62), RSTPRPLPPLPTTR (SEQ ID NO. 67), GILAPPVPPRNTR (SEQ ID NO. 63), VLKRPLPIPPVTR (SEQ ID NO. 64), GPHRRLPPTPATR (SEQ ID NO. 65), and ANPSPATRPLPTR (SEQ ID NO. 66).

Phage clones are also disclosed, along with the amino acid sequences that are responsible for SH3 domain binding. These phage clones are identified in Figure 5.

10 In other embodiments of the present invention, SH3 domain-binding peptides are contemplated which have a total of 11, 13, 14, 18, 20, 22, 23, 25, 30, 36, 38 or 45 amino acid residues.

The peptides of the present invention, having been
15 disclosed herein, may be prepared by any number of practicable methods, including but not limited to solution-phase synthesis, solid-phase synthesis, protein expression by a transformed host, cleavage from a naturally-derived, synthetic or semi-synthetic polypeptide, or a combination of
20 these techniques.

The SH3 binding peptides exhibit a wide range of biological activity which includes the enhancement (or inhibition, depending on the particular peptide or the nature of the peptide's target molecule, in this case a protein
25 bearing an SH3 domain) of the natural function or biological activity of the peptide's target molecule. For example, the interaction of the binding peptide of the present invention could result in the modulation of the oncogenic activity of the target molecule bearing the SH3 domain. If the target
30 molecule has, in turn, a natural binding partner or ligand, the peptides of the present invention may also exhibit antagonistic or agonistic activity in relation to the biological activity of the natural binding partner.

Thus, it is an object of the present invention to
35 provide a method of activating Src or Src-related protein in tyrosine kinases by administering an effective amount of the SH3 domain-binding peptides generally described herein. The

intensity of the immune response can thus be stimulated, for example, by the increased production of certain lymphokines, such as TNF-alpha and interleukin-1. As is generally known to those of ordinary skill in the art, a more intense immune response may be in order in certain conditions, such as in combating a particularly tenacious infection, viral or otherwise, or a malignancy.

Furthermore, in a specific embodiment of the present invention, a conjugate compound is contemplated which comprises the peptide of the present invention and a second chemical moiety. The second chemical moiety can be selected from a wide variety of chemical compounds including the peptide itself. Typically, however, the second chemical moiety is selected to be other than the peptide of the present invention, including but not limited to an amino acid, a peptide other than an SH3 binding peptide of the present invention, a polypeptide or protein (i.e., the conjugate is a fusion protein), a nucleic acid, a nucleoside, a glycosidic residue (i.e., any sugar or carbohydrate), a label or image-enhancing agent (including metals, isotopes, radioisotopes, chromophores, fluorophores (such as FITC, TRITC, and the like), and enzyme substrates), a drug (including synthetic, semisynthetic, and naturally-occurring compounds), small molecules (e.g., biotin, hormones, factors) and the like.

The peptide of the present invention can be conjugated to the second chemical moiety either directly (e.g., through appropriate functional groups, such as an amine or carboxylic acid group to form, for example, an amine, imine, amide, ester, acyl or other carbon-carbon bond) or indirectly through the intermediacy of a linker group (e.g., an aliphatic or aromatic polyhydroxy, polyamine, polycarboxylic acid, polyolefin or appropriate combinations thereof). Moreover, the term "conjugate," as used herein, is also meant to encompass non-covalent interactions, including but not limited to ionic, affinity or other complexation interactions. Preferably, such other non-covalent

interactions provided and finable, most preferably, is a labile chemical conjugate species.

As described further herein, the peptides of the present invention have been shown to localize within certain cellular compartments which contain Src or Src-related proteins. Consequently, the above-described conjugate can be utilized as a delivery system for introduction of a drug to cells, tissues or organs that include SH3 domain-containing proteins.

10 It should also be pointed out that the present invention seeks to provide a recombinant construct comprising a nucleic acid or its complement that includes codons or nucleotide sequences encoding a peptide having a region that binds to an SH3 domain, preferably the Src SH3 domain. The recombinant
15 nucleic acid may be a DNA or RNA polynucleotide.

In a specific embodiment, the present invention contemplates a recombinant construct which is a transforming vector. Such vectors include those well known to those of ordinary skill in the art, which effect the transfer or
20 expression of the nucleotide sequence after introduction to a host, such as recombinant plasmid, phage or yeast artificial chromosome. These vectors may be closed circular loops or they may be linearized. The vectors contemplated include those that exist extrachromosomally after host transformation
25 or transfection, as well as those that integrate within or even displace portions of the host chromosome. The vectors may be introduced to the cell with the help of transfection aids or techniques well-known in the art. For example, these aids or techniques may take the form of electroporation, use
30 of calcium chloride, calcium phosphate, DEAE dextran, liposomes or polar lipid reagents known as LIPOFECTIN or LIPOFECTAMINE. In addition, the present invention contemplates the direct introduction of the desired nucleic acid to the host cell, for instance, by injection.

35 Transformed host cells are also obtained by the methods of the present invention which are capable of reproducing the polynucleotide sequences of interest and/or expressing the

c rresponding peptid products. A vari ty of h sts are c ntemplat d, including prokary tic and eukaryotic hosts. In particular, bacterial, viral, yeast, animal, and plant cells are potentially transformable hosts. Thus, a method is
5 disclosed to obtain a transformed host cell that can produce, preferably secrete, a peptide having a region that binds to an SH3 domain comprising (a) providing an expression vector, preferably a secretory expression vector, comprising a nucleotide sequence encoding at least one copy of a peptide
10 having a region that binds to an SH3 domain; and (b) introducing the vector to a competent host cell.

The peptides, thus produced, may then be introduced to cells, tissues, organs, or administered to the subject for the purpose of modulating the biochemical activity of the SH3
15 domain-containing proteins present therein. Accordingly, in specific embodiments of the present invention, compositions are provided which comprise an SH3 domain-binding peptide, including a core sequence and flanking sequences, and a suitable carrier.

20 The compositions contemplated by the present invention may also include other components, from those that facilitate the introduction or administration of the compositions to those that have their own innate activity, such as a prophylactic, a diagnostic or a therapeutic action. Such
25 innate activity may be distinct from that of the peptides of the present invention or be complementary thereto. In any event, the compositions of the present invention include those that are suitable for administration into mammals, including humans. Preferably, the compositions (including
30 necessarily the carrier) of the present invention are sterile, though others may need only be cosmetically, agriculturally or pharmaceutically acceptable. Still other compositions may be adapted for veterinary use.

The compositions, including the drug delivery systems
35 d scribed h r in, are contemplat d to be administered in a variety of ways, such as parent rally, orally, ent rally, t pically or by inhalation. Th c mpositions may also be

administered intranasally, pthalmically or intravaginally. Furtherm r , the c mpositions f the inv nti n can tak several forms, such as solids, gels, liquids, a r s ls or patches.

5 In another embodiment of the present invention a method is provided of identifying a peptide having a region that binds to an SH3 domain comprising: (a) providing an immobilized target protein comprising an SH3 domain; (b) incubating the immobilized target protein with an aliquot
10 taken from a phage-displayed random peptide library, which library includes peptides having a random sequence of ≥ 8 amino acid residues; (c) washing unbound phage from the immobilized target protein; (d) recovering the phage bound to the immobilized target protein; and (e) determining the
15 relevant nucleotide sequence of said binding phage nucleic acid and deducing the primary sequence corresponding to the SH3 domain-binding peptide. Preferably, the method further comprises amplifying the titer of the recovered phage and repeating the steps of incubation, washing and recovery to
20 provide SH3 domain-binding peptide-enriched phage.

Any other mode by which the peptide library, random or otherwise, can be "displayed" can be utilized in the present invention, however. Moreover, the present applicants believe that longer random peptide sequences (e.g., >6 amino acid
25 residues, preferably >10 , and most preferably, >12) provide not only much greater diversity but also a richer degree of secondary structure conducive to binding activity. If the random region of the peptide is less than or equal to an 8-mer, it should preferably not be cyclized.

30

5.2. Preparation of Random Peptide Libraries

The preparation and characterization of the preferred phage-displayed random peptide libraries have been described elsewhere. See, for example, Kay, B.K. et al. in
35 Gene (1992) 128:59-65, for a description of the preparation of th phage-displayed rand m peptide library known as TSAR-9, more below. In particular, by cloning deg n rat

ligonucleotides of fixed length into bacteriophage vectors, recombinant libraries of random peptides can be generated which are expressed at the amino-terminus of the pIII protein on the surface of M13 viral particles. (There are 3-5 copies of the pIII-fusion on the surface of each particle.) Phage display offers several conveniences: first, the expressed peptides are on the surface of the viral particles and accessible for interactions; second, the recombinant viral particles are stable (i.e., can be frozen, exposed to pH extremes); third, the viruses can be amplified; and fourth, each viral particle contains the DNA encoding the recombinant genome. Consequently, these libraries can be screened by isolating viral particles that bind to targets. The isolates can be grown up overnight, and the displayed peptide sequence responsible for binding can be deduced by DNA sequencing.

These libraries have approximately $>10^8$ different recombinants, and nucleotide sequencing of the inserts suggests that the expressed peptides are indeed random in amino acid sequence. These libraries are referred to herein as TSAR libraries, where TSAR stands for Totally Synthetic Affinity Reagents. The preparation of the TSAR libraries are described further below.

5.3. SH3 Binding Clones And Their Characteristics

Accordingly, peptides have been isolated from an unconstrained random peptide library which exhibit a binding affinity for SH3 domains. Furthermore, the binding affinities exhibited by the disclosed peptides differ in their selectivities with certain peptides showing comparable binding affinities for SH3 domains derived from different proteins, while others manifest greater affinities for specific SH3 domains.

The amino acid sequence of various peptides isolated by the present method are listed in Figure 5. As can be seen from this list, certain groups of SH3 domain binding peptides are isolated from three separate random peptide libraries, each based on a different type of random peptide insert, all

displayed at the amino-terminus of the pIII protein on the surface of M13 viral particles. Ten clones were isolated from the R8C library, seven from the TSAR-12 library, and seven from the TSAR-9 library. The sequences are presented to highlight the particular amino acid residues believed to bind directly to the SH3 domain, as well as to point out the remaining amino acid residues of the random insert and the viral flanking sequences and complementary site amino acid residues common to each group of clones. The frequency with which each particular clone is found in each library is also indicated in Figure 5. Thus, clones T12.SRC3.1 and T12.SRC3.2 are by far the most abundant clones found among the three libraries.

Interestingly, all the binding peptides are found to have the proline-rich amino acid residue motif, which is apparently responsible for binding, the motif being located predominantly at the C-terminal end of the insert, although each clone also contains an insert at the N-terminal end. The significance of this observation is not presently understood, although this finding may indicate the possible importance of the C-terminal viral flanking sequences in SH3 domain binding.

Indeed, a synthetic peptide bearing only the core consensus sequence RPLPPLP (SEQ ID NO:9) was less effective in binding to target SH3 domains than synthetic peptides that also included additional amino acid residues flanking the core sequences. Thus, 13-mers and 14-mers having the sequences RSTPRPLPMLPTTR (SEQ ID NO:62), RSTPRPLPPLPTTR (SEQ ID NO:67), GILAPPVPPRNTTR (SEQ ID NO:63), GPHRRPLPPTPATR (SEQ ID NO:65), and VLKRPLPIPPVTR (SEQ ID NO:64) have been prepared and shown to bind to SH3 domains, such as those of Src and Yes, much more avidly than the 7-mer, RPLPPLP (SEQ ID NO:9). The 13-mer ANPSPATRPLPTR (SEQ ID NO:66) has been shown to have binding affinities comparable to the core consensus sequence. In each case, the 13-mers comprise a 7-mer "core" sequence plus additional amino acid residues

flanking sam , s me of which additional amino acid residues are c ntributed by th viral flanking s quences.

Thus, in on embodim nt of the present inventi n, a 7-mer core includes a consensus motif of the formula RXLPφφP
5 (SEQ ID NO:71), wherein R is arginine, L is leucine, P is proline, X represents any amino acid except cysteine and φ represents a hydrophobic amino acid residue. By "hydrophobic amino acid residue," the applicants mean to include F, Y, W, V, A, I, L, P or M, each letter representing the standard
10 one-letter designation for the corresponding amino acid residue.

Furthermore, a preferred 9-mer peptide comprising two additional amino acids on the C-terminal end of the core sequence is envisioned having a consensus motif of the
15 formula RXLPφφPXψ. In this preferred 9-mer consensus motif, the symbol ψ represents a hydrophilic amino acid residue, except cysteine. By "hydrophilic amino acid residue," the applicants mean to include K, R, H, D, E, N, Q, T, S or C, and the other symbols are as defined above. For the purpos s
20 of the present invention, a glycine residue (G) may be considered either a hydrophobic or a hydrophilic amino acid residue. The one-letter symbols B and Z, which stand for N or D and Q or E, respectively, are considered hydrophilic amino acid residues.

25 Particular 13-mer peptides of the present invention include those listed, below. It is noted, however, that not all the following 13-mer peptides correlate strictly to or comply with the preferred 9-mer consensus motif, described above. Those peptides that do not comply (indicated in
30 italics, with the non-complying amino acid residues underscored) can, thus, be described as "resembling" those that do comply (indicated in normal type) with the preferred 9-mer consensus motif: PGFRELPLPPSR (SEQ ID NO:72),
AQSRLPIPPETR (SEQ ID NO:73), VLKRPLPIPPVTR (SEQ ID NO:64),
35 *PPNS*SPLPLPLTHL (SEQ ID NO:74), TGRGPLPLPNDS (SEQ ID NO:75),
YSTRPVPPITRPS (SEQ ID NO:76), *SHK*SRLPLPTRP (SEQ ID NO:77),
YRFRALPSPPSAS (SEQ ID NO:78), GPHRRLPPTPATR (SEQ ID NO:65),

LAQRQLPPTPGRD (SEQ ID NO:79), ALQRRLPRTPPPA (SEQ ID NO:80),
 PATRPLPTRPSRT (SEQ ID NO:81), YSTRPLPSRPSRT (SEQ ID NO:82),
 XPGRIILLPSEPR (SEQ ID NO:83), SGGILAPPVPPRN (SEQ ID NO:84),
 RSTRPLPILPRTT (SEQ ID NO:85), STPRPLPMLPTTR (SEQ ID NO:86),
 5 STNRPLPMIPTTR (SEQ ID NO:87), RSTRPLPSLPITT (SEQ ID NO:88),
 STSRPLPSLPPTTR (SEQ ID NO:89), RSTRSLPPLPPTT (SEQ ID NO:90),
 RSTRQLPIPTTT (SEQ ID NO:91), STPRPLPLIPTTP (SEQ ID NO:92),
 RSTRPLPPTPLTT (SEQ ID NO:93), and RSTRPQPPPPITT (SEQ ID
 NO:94). Accordingly, other peptides not specifically
 10 disclosed, which either comply with or "resemble" the
 preferred 9-mer consensus motif, can be readily envisioned by
 those of ordinary skill in the art and are considered to be
 equivalent to those that are specifically disclosed above.
 In particular, non-compliance at positions 1 (S, G, and I, in
 15 place of R, are tolerated), 3 (V, A, and Q, in place of L,
 are tolerated), 4 (L, in place of P, is tolerated), 5
 (hydrophilic amino acid residues, S, R, and T, are tolerated
 in place of a hydrophobic amino acid residue), 6 (hydrophilic
 amino acid residues, R and T, are tolerated in place of a
 20 hydrophobic amino acid residue), 7 (T, and S, in place of P,
 are tolerated), and 9 (P and A are tolerated in place of a
 hydrophilic amino acid residue) have been observed.

5.3.1. Binding Specificities

25 It has been discovered that certain of the
 binding peptides disclosed have a greater relative binding
 affinity for one SH3 domain over another. Referring now to
 Figure 8, the relative binding affinities of the various
 peptides described above toward different SH3 domain targets
 30 are graphically presented. As one can see, the relative
 binding affinities of the respective peptides can differ by
 orders of magnitude. Thus, as shown in Figure 8, the peptid
 GPHRRLPPTPATR (SEQ ID NO:65), having the relevant sequence of
 the phage clone identified as T12.SRC3.3, is specific to Src
 35 family SH3 domains, including, but not limited to, Src, Yes,
 Lck, Hck, Fgr, Fyn, and Lyn. This SH3 binding peptide has
 little affinity for SH3 domains derived from PLC γ or Grb2.

On the other hand, the peptide GILAPPVPPRNTR (SEQ ID NO:63), corresponding to the relevant sequence of the phage clone T12.SRC3.1, which is one of the most abundant binding clones found by the present method, binds generically to a broad range of SH3 domains, including Src, PLC γ , and Grb2.

On an intermediate level, the present invention has also uncovered a peptide, VLKRPLPIPPVTR (SEQ ID NO:64), corresponding to the relevant sequence of the phage clone T12.SRC3.6, which is Src preferential; that is, this peptide exhibits strong binding affinities for members of the Src family, some binding affinities for Grb2 proteins, but little binding affinities for PLC γ domains. The peptide ANPSPATRPLPTR (SEQ ID NO:66), corresponding to the relevant sequence of the phage clone T12.SRC3.2, also exhibits Src family specificity similar to GPHRRLPPTPATR (SEQ ID NO:65). The peptides RSTPRPLPMLPTTR (R8C.YES3.5; SEQ ID NO:62) and RSTPRPLPPLPTTR (representative consensus motif; SEQ ID NO:67) are highly specific for SH3 domain of Src, Yes, and other Src-related proteins.

20

5.4. Further Discussion of Binding Experiments

At the outset it is apparent that the binding affinity of certain peptides to the SH3 domain of Src and Src-related proteins is governed by more than just the presence of the preferred core consensus sequences, RLPPLP (SEQ ID NO:9) or RPLPMLP (SEQ ID NO:95; i.e., RLP(P/M)LP, SEQ ID NO:96). Thus, while the synthetic peptides RSTPRPLPMLPTTR (R8C.YES3.5; SEQ ID NO:62) and RSTPRPLPPLPTTR (consensus; SEQ ID NO:67) exhibit a strong specific binding affinity for Src SH3, the other synthetic peptides tested also exhibited an avid binding affinity to SH3 domains relative to the 7-mer, RLPPLP (SEQ ID NO:9). These other peptides, GILAPPVPPRNTR (SEQ ID NO:63), VLKRPLPIPPVTR (SEQ ID NO:64), GPHRRLPPTPATR (SEQ ID NO:65), and ANPSPATRPLPTR (SEQ ID NO:66), sport core sequences and flanking sequences that do not closely adhere to the preferred core consensus sequences. Thus, these results suggest that binding affinity

t SH3 domains is govern d to a larg ext nt by the nature of
th amino acid residu s flanking th c re 7-m r sequ nce.

The binding charact ristics f Src SH3-s lected p ptides
was determined using synthetic biotinylated peptides

5 corresponding to the sequences displayed by Src SH3-selected
phage. These biotinylated peptides were assayed for direct
binding to immobilized Src SH3-GST. Each of the five
library-derived peptides tested were found to bind to Src
SH3-GST and Yes SH3-GST over background (Figure 8).

10 Furthermore, a strong correlation was observed between the
similarity of a given peptide to the preferred core consensus
sequence RPLP(P/M)LP and the peptide's affinity for Src SH3-
GST. The core sequence of the clone T12.SRC3.1

(GILAPPVPPRNTR; SEQ ID NO:63) appears to provide more generic
15 SH3 domain-binding characteristics.

Experiments comparing the relative binding of various
phage clones to SH3 domains taken from a variety of proteins
demonstrated the preference of these clones for Src and Src-
related SH3 domains over SH3 domains taken from other
20 proteins.

It was further found that while the 7-mer having the
consensus sequence RPLPPLP (SEQ ID NO:9) bound to Src SH3-GST
only weakly, peptides comprising the consensus sequence
flanked by residues encoded by one of the Src SH3-selected
25 clones (R8C.YES3.5), RSTP (SEQ ID NO:97) at the N-terminal
end and TTR at the C-terminal end, bound significantly better
than any of the peptides tested (Figure 7). Thus, as stat d
previously, sequences that flank the RPLP(P/M)LP (SEQ ID
NO:96) core appear to be important contributors to SH3
30 binding. It is further surmised that a peptide having or
resembling the sequence RSTPAPPVPPRTTR (SEQ ID NO:98) should
exhibit strong but generic binding to a variety of SH3
domains.

Similarly, it is observed that most of the Src SH3-
35 binding m tifs are located n ar the carboxy-t rminus of the
random peptides, adjac nt t s quences which ar fix d in
every clone (Figure 5). The exc ptional clones t nd to

possess sequences that resemble motifs that include fixed flanking sequences. This clustering contrasts with previous results, in which binding motifs are distributed throughout the random peptide. Kay, B.K., et al., in Gene (1993) 5 128:59-65.

The binding of the library-derived Src SH3-binding peptides was compared to that of peptides corresponding to proline-rich regions of natural proteins. Peptides corresponding to SH3-binding regions in human PI-3' Kinase 10 (KISPPTPKPRPPRPLPV; SEQ ID NO:69) and human SOS1.20 (GTVEPVPPPVPRRRPESA; SEQ ID NO:68), as well as a proline-rich region of the cytoskeletal protein vinculin (LAPPKPPLPEGEV; SEQ ID NO:70), bound Src SH3 less well than the library-derived peptides (Figure 7).

15 As mentioned above, the relative specificity of binding was explored. Thus, the relative binding of Src SH3-select d peptides to equal amounts of GST fusions to SH3 domains from different proteins was determined (Figure 8). While all of the library-derived peptides bound the Src and Yes SH3 20 domains almost equally well, none of the peptides (with the exception of peptide T12.SRC3.1, the most divergent peptide tested) bound the SH3 domains of Grb2, Crk, Abl or PLC γ 1 appreciably. Thus, the library-derived peptides, in contrast with a peptide derived from SOS1, exhibit SH3 binding that is 25 relatively specific for Src-family members.

Next, it was determined whether the binding to the Src SH3 domain was qualitatively like the interactions of the SH3 domain and natural proteins found in cell lysates. Thus, radiolabeled proteins were prepared from NIH 3T3 cell lysates 30 and chromatographed over Src SH3-GST immobilized on glutathione linked Sepharose. SDS-PAGE shows that a number of proteins can be affinity purified in this manner. The synthesized peptides bind quite well to the Src SH3 domain, as they can compete the binding of radiolabeled proteins from 35 cell lysates to immobilized Src-GST, with an IC₅₀ of 1-10 mM (Figure 9). In conclusion, the peptides can efficiently

black th interacti n f cellular proteins with Src SH3 in vitro.

Moreover, *Xenopus laevis* oocytes injected with mRNA encoding constitutively active Src undergo progesterone-induced maturation at an accelerated rate relative to oocytes injected with water or c-Src mRNA. Unger, T.F. and Steele, R.E. in Mol. Cell. Biol. (1992) 12:5485-5498. To explore the ability of the library-derived Src SH3-binding peptides to exert a biochemical effect in vivo, the influence of the peptides on the maturation of *Xenopus laevis* oocytes was examined. Hence, stage VI oocytes were injected with peptide, exposed to progesterone, and scored for germinal vesicle breakdown. Figure 10 shows that the rate of maturation was accelerated by approximately one hour when oocytes were injected with the SH3-binding peptide consisting of RPLPPLP (SEQ ID NO:9) flanked by residues from clone T12.SRC3.6 (VLKRPLPIPPVTR; SEQ ID NO:64), but not with water or a peptide corresponding to a proline-rich segment of vinculin (LAPPKPPLPEGEV; SEQ ID NO:70) as controls. The magnitude of this effect is roughly equivalent to that seen with injection of mRNA encoding constitutively active Src. See, e.g., Figure 3B in Unger, T.F. and Steele, R.E., supra. This result suggests that the library-derived Src SH3-binding peptide is effectively relieving an inhibitory effect of the Src SH3 domain upon Src PTK activity. This model is consistent with a number of studies which have demonstrated an inhibitory effect of the Src SH3 domain upon Src kinase and transforming activity. See, e.g., Okada, M., et al., supra; Murphy, S.M., et al., supra; and Superti-Furga, G., et al., supra.

5.5. Diagnostic And Therapeutic Agents Based On SH3 Binding Peptides and Additional Methods of Their Use

As already indicated above, the present invention also seeks to provide diagnostic, prophylactic, and

therapeutic agents based on the SH3 binding peptides described herein.

In one embodiment, diagnostic agents are provided, preferably in the form of kits, comprising an SH3 domain-binding peptide and a detectable label conjugated to said peptide directly, indirectly or by complexation, said peptide comprising: (i) a core sequence motif of the formula RXLP ϕ ϕ P (SEQ ID NO:71), wherein X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue, including F, Y, W, V, A, I, L, P, M or G, each letter representing the standard one-letter designation for the corresponding amino acid residue; and (ii) two or more additional amino acid residues flanking said core sequence at its C-terminal end, N-terminal end or both.

The diagnostic agents of the present invention can be used to detect the presence of SH3 domains of a generic or specific type in cells, tissues or organs either *in vitro* or *in vivo*. For *in vivo* applications, the diagnostic agent is preferably mixed with a pharmaceutically acceptable carrier for administration, either enterally, parenterally or by some other route dictated by the needs of the particular application.

In a particular embodiment, for example, an assay based on a fusion product is contemplated which comprises a Src SH3 domain-binding peptide of the invention and a substrate for deregulated or "activated" Src. For instance, a muscle biopsy, taken from a subject suspected of being infected by the Rous sarcoma virus, can be treated with an effective amount of the fusion product. By subsequent analysis of the degree of conversion of the substrate, one can potentially detect infection by the Rous sarcoma virus in the subject, particularly mammals, especially chickens. The presence of the retrovirus, which causes the expression of deregulated or "activated" Src, may thus be indicated by unusually high levels of Src as revealed by large amounts of the converted substrate. See, for example, Paxton, W.G. et al., in Biochem. Biophys. Res. Commun. (1994) 200(1):260-267

(detection of phosphorylated tyrosine and serine residues of angiotensin II AT1 receptor, a substrate of Src family tyrosine kinases); another suitable substrate may be the protein p68 (Fumagalli, S. et al., in Nature (1994) 368(6474):871-874; Taylor, S.J. and Shalloway, D., in Ibid. at 867-871.

Alternatively, the enzyme can be isolated by selective binding to a form of the SH3 domain-binding peptides of the present invention (e.g., biotin-peptide conjugate). After
10 isolation of the protein-peptide conjugate complex (e.g., on a column comprising streptavidin), the activity of the enzyme can then be assayed by conventional methods to determine its level of protein kinase activity which can be taken as an indication of the presence of the deregulated or "activated"
15 form of the enzyme. An assay for Src kinase has been described by Klinz and Maness, in Neuroprotocols (a companion to Neuroscience) (1992) 1(3):224-231.

Moreover, the diagnostic agents of the invention can also serve as imaging agents of cells, tissues or organs,
20 especially those that contain proteins with an SH3 domain. For example, neural cells (e.g., neurons, other areas of the brain), osteoclasts, osteoblasts, platelets, immune cells, and other dividing cells are known to express or contain proteins with SH3 domains. Thus, an image can be taken of
25 portions of the body to serve as a baseline for subsequent images to detect physiologic or biochemical changes in the subject's body. For instance, changes in the condition of cellular levels of Src or a transformation of the cellular Src to an "activated" form may be detected using the
30 diagnostic or imaging agents of the present invention.

Accordingly, it has been demonstrated that an SH3-binding peptide tagged with a fluorescence emitter can provide an image of the cytoskeleton. The images are presented in Figure 11. As can be seen from Figure 11,
35 panels A, B, and C show the fluorescence image that is obtained on treating NIH 3T3 fibroblasts with SH3 domain-binding peptides modified to include a fluorescent tag. In

sharp contrast, panel D shows only a dark image that is produced when the cells are treated with a proline-rich segment of vinculin as a control.

In another embodiment, an SH3 domain-binding peptide-horseradish immunoperoxidase complex or related immunohistochemical agent could be used to detect and quantitate specific receptor molecules in tissues, serum or body fluids. In particular, the present invention provides useful diagnostic reagents for use in immunoassays, Southern or Northern hybridization, and *in situ* assays. Accordingly, the diagnostic agents described herein may be suitable for use *in vitro* or *in vivo*.

In addition, the diagnostic or imaging agent of the present invention is not limited by the nature of the detectable label. Hence, the diagnostic agent may contain one or more such labels including, but not limited to, radioisotope, fluorescent tags, paramagnetic substances, heavy metals, or other image-enhancing agents. Those of ordinary skill in the art would be familiar with the range of label and methods to incorporate or conjugate them into the SH3 domain-binding peptide to form diagnostic agents.

In yet a further embodiment, pharmaceutical compositions are provided comprising an SH3 domain-binding peptide and a pharmaceutically acceptable carrier. In a specific embodiment of the invention, the pharmaceutical composition is useful for the modulation of the activity of SH3 domain-containing proteins. By "modulation" is meant either inhibition or enhancement of the activity of the protein target. Accordingly, a pharmaceutical composition is disclosed comprising an SH3 domain-binding peptide and a pharmaceutically acceptable carrier, said peptide comprising: (i) a 9-mer sequence motif of the formula RXLP ϕ ϕ PX ψ (SEQ ID NO:10), wherein X represents any amino acid except cysteine, ϕ represents a hydrophobic amino acid residue, and wherein ψ is a hydrophilic amino acid residue except cysteine, each letter representing the standard one-letter designation for the corresponding amino acid residue; and, optionally, (ii)

additional amino acid residues flanking the 9-mer sequence at its C-terminal end, N-terminal end or both, up to a total of 45 amino acid residues, including said 9-mer sequence.

Preferably, the peptide comprises at least one, more preferably at least two, and most preferably at least three additional amino acids flanking the 9-mer sequence.

As stated above, the therapeutic or diagnostic agents of the invention may also contain appropriate pharmaceutically acceptable carriers, diluents and adjuvants. Such pharmaceutical carriers can be sterile liquids, such as water and oils including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, magnesium carbonate, magnesium stearate, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. These compositions can take the form of solutions, suspensions, tablets, pills, capsules, powders, sustained-release formulations and the like. Suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin.

Such compositions will contain an effective therapeutic amount of the active compound together with a suitable amount of carrier so as to provide the form for proper administration to the subject. While intravenous injection is a very effective form of administration, other modes can be employed, including but not limited to intramuscular, intraperitoneal, and subcutaneous injection, and oral, nasal, enteral, and parenteral administration.

The therapeutic agents and diagnostic agents of the instant invention are used for the treatment and/or diagnosis

of animals, and more preferably, mammals including humans, as well as dogs, cats, horses, cows, pigs, guinea pigs, mice and rats. Accordingly, the methods contemplated in the present invention, include, but are not limited to, a method of modulating, i.e., inhibiting or enhancing, bone resorption in a mammal (see, e.g., Hall, T.J., in Biochem. Biophys. Res. Commun. (1994) 199(3):1237-44), a method of disrupting protein tyrosine kinase-mediated signal transduction pathways or a method of regulating the processing, trafficking or translation of RNA in a cell by introducing or administering an effective amount of an SH3 domain-binding peptide of the present invention (see, e.g., Taylor, S.J. and Shalloway, D., *supra*).

The diagnostic or therapeutic agents of the present invention can be modified by attachment to soluble macromolecules such as proteins, polysaccharides, or synthetic polymers. For example, the peptide could be coupled to styrene-maleic acid copolymers (see, e.g., Matsumura and Maeda, Cancer Res. (1986) 46:6387), methacrylamide copolymers (Kopeček and Duncan, J. Controlled Release (1987) 6:315), or polyethylene glycol (PEG) (e.g., Hershfield and Buckley, N. Engl. J. Med. (1987) 316:589; Ho et al., Drug Metab. Dispos. (1986) 14:349; Chua et al., Ann. Intern. Med. (1988) 109:114). The agents, if desired, are further targeted by attachment to an antibody, especially a monoclonal antibody. Such antibodies include but are not limited to chimeric, single chain, Fab fragments, and Fab expression libraries. In one embodiment the agent is coupled to the macromolecule via a degradable linkage so that it will be released *in vivo* in its active form.

In another embodiment, the therapeutic or diagnostic agent may be delivered in a vesicle, in particular a liposome. See, Langer, Science (1990) 249:1527-1533; Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York (1989) pp. 353-365; Lopez-Berestein, *ibid.*, pp. 317-327.

In yet another embodiment, the therapeutic or *in vivo* diagnostic agent can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, *supra*; Sefton, CRC Crit. Ref. Biomed. Eng. (1987) 14:201; 5 Buchwald et al., Surgery (1980) 88:507; Saudek et al., N. Engl. J. Med. (1989) 321:574). In another embodiment, polymeric materials may be used (see Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida, 1974; Controlled Drug Bioavailability, Drug 10 Product Design and Performance, Smolen and Ball (eds.) Wiley, New York 1984; Raner and Peppas, J. Macromol. Sci. Rev. Macromol. Chem. (1983) 23:61; see, also, Levy et al., Science (1985) 228:190; During et al., Ann. Neurol. (1989) 25:351; Howard et al., J. Neurosurg. (1989) 71:105). In a preferred 15 embodiment, a controlled release system may be placed next to the therapeutic target, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in Medical Applications of Controlled Release, *supra*, (1984) 2:115-138). It will be recognized by one of ordinary skill in the art that a 20 particular advantage of the invention is that a peptide will not be subject to the problems of denaturation and aggregation associated with proteins held in the warm, moist environment of a body in a controlled release system.

Other controlled release systems are discussed in the 25 review by Langer, in Science (1990) 249:1527-1533.

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6. EXAMPLES

6.1. Preparation of the TSAR-9 Library

6.1.1. Synthesis and Assembly of Oligonucleotides

Figure 1 shows the formula of the oligonucleotides and the assembly scheme used in construction of the TSAR-9 library. The oligonucleotides were synthesized with an applied Biosystems 380a synthesizer (Foster City, CA), and the full-length oligonucleotides were purified by HPLC.

Five micrograms of each of the pair of oligonucleotides were mixed together in buffer (10 mM Tris-HCl, pH 8.3, 15 mM KCl, 0.001% gelatin, 1.5 mM magnesium chloride), with 0.1 % Triton X-100, 2 mM dNTP's, and 20 units of Taq DNA polymerase. The assembly reaction mixtures were incubated at 72 °C for 30 seconds and then 30 °C for 30 seconds; this cycle was repeated 60 times. It should be noted that the assembly reaction is not PCR, since a denaturation step was not used. Fill-in reactions were carried out in a thermal cycling device (Ericomp, LaJolla, CA) with the following protocol: 30 seconds at 72 °C, 30 seconds at 30 °C, repeated for 60 cycles. The lower temperature allows for annealing of the six base complementary region between the two sets of the oligonucleotide pairs. The reaction products were phenol/chloroform extracted and ethanol precipitated. Greater than 90% of the nucleotides were found to have been converted to double stranded synthetic oligonucleotides.

After resuspension in 300 µL of buffer containing 10 mM Tris-HCl, pH 7.5, 1 mM EDTA (TE buffer), the ends of the oligonucleotide fragments were cleaved with Xba I and Xho I (New England BioLabs, Beverly, MA) according to the supplier's recommendations. The fragments were purified by 4% agarose gel electrophoresis. The band of correct size was removed and electroeluted, concentrated by ethanol precipitation and resuspended in 100 µL TE buffer. Approximately 5% of the assembled oligonucleotides can be expected to have internal Xho I or Xba I sites; however, only

th full-length molecules were used in the ligation step of the assembly scheme. The concentration of the synthetic oligonucleotide fragments was estimated by comparing the intensity on an ethidium bromide stained gel run along with appropriate quantitated markers. All DNA manipulations not described in detail were performed according to Maniatis, *supra*.

To demonstrate that the assembled enzyme digested oligonucleotides could be ligated, the synthesized DNA fragments were examined for their ability to self-ligate. The digested fragments were incubated overnight at 18 °C in ligation buffer with T4 DNA ligase. When the ligation products were examined by agarose gel electrophoresis, a concatamer of bands was visible upon ethidium bromide staining. As many as five different unit length concatamer bands (i.e., dimer, trimer, tetramer, pentamer, hexamer) were evident, suggesting that the synthesized DNA fragments were efficient substrates for ligation.

6.1.2. Construction of Vectors

The construction of the M13 derived phage vectors useful for expressing a TSAR library has been recently described (Fowlkes, D. et al. BioTech. (1992) 13:422-427). To express the TSAR-9 library, an M13 derived vector, m663, was constructed as described in Fowlkes. The m663 vector contains the pIII gene having a c-myc-epitope, i.e., as a stuffer fragment, introduced at the mature N-terminal end, flanked by Xho I and Xba I restriction sites (see also, Figure I of Fowlkes).

6.1.3. Expression of the TSAR-9 Library

The synthesized oligonucleotides were then ligated to Xho I and Xba I double-digested m663 RF DNA containing, the pIII gene (Fowlkes) by incubation with ligase overnight at 12 °C. More particularly, 50 ng of vector DNA and 5 ng of the digested synthesized DNA and was mixed together in 50 µL ligation buffer (50 mM Tris, pH 8.0, 10 mM

MgCl₂, 20 mM DTT, 0.1 mM ATP) with T4 DNA ligase. After overnight ligation at 12°C, the DNA was concentrated by ethanol precipitation and washed with 70% ethanol. The ligated DNA was then introduced into *E. coli* (DH5αF'; GIBCO 5 BRL, Gaithersburg, MD) by electroporation.

A small aliquot of the electroporated cells was plated and the number of plaques counted to determine that 10⁸ recombinants were generated. The library of *E. coli* cells containing recombinant vectors was plated at a high density 10 (-400,000 per 150 mm petri plate) for a single amplification of the recombinant phage. After 8 hr, the recombinant bacteriophage were recovered by washing each plate for 18 hr with SMG buffer (100 mM NaCl, 10 mM Tris-HCl, pH 7.5, 10 mM MgCl₂, 0.05% gelatin) and after the addition of glycerol to 15 50% were frozen at -80 °C. The TSAR-9 library thus formed had a working titer of $\sim 2 \times 10^{11}$ pfu/ml.

6.2. Preparation of TSAR-12 Library

Figure 2 shows the formula for the synthetic 20 oligonucleotides and the assembly scheme used in the construction of the TSAR-12 library. As shown in Figure 2, the TSAR-12 library was prepared substantially the same as the TSAR-9 library described in Section 6.1 above with the following exceptions: (1) each of the variant non-predicted 25 oligonucleotide sequences, i.e., NNB, was 30 nucleotides in length, rather than 54 nucleotides; (2) the restriction sites included at the 5' termini of the variant, non-predicted sequences were *Sal* I and *Spe* I, rather than *Xho* I and *Xba* I; and (3) the invariant sequence at the 3' termini to aid 30 annealing of the two strands was GCGGTG and CGCCAC rather than CCAGGT and GGTCCA (5' to 3').

After synthesis including numerous rounds of annealing and chain extension in the presence of dNTP's and *Tag* DNA polymerase, and purification as described above in Section 35 6.1.1, the synthetic double stranded, oligonucleotide fragments were digested with *Sal* I and *Spe* I restriction enzymes and ligated with T4 DNA ligase to the nucleotide

sequence encoding the M13 pIII gene contained in the m663 vector to yield a library of TSAR- expression vectors as described in Sections 6.1.2 and 6.1.3. The ligated DNA was then introduced into *E. coli* (DH5 α F'; GIBCO BRL, Gaithersburg, MD by electroporation. The library of *E. coli* cells were plated at high density (~400,000 per 150 mm petri plate) for amplification of the recombinant phage. After about 8 hr, the recombinant bacteriophage were recovered by washing, for 18 hr with SMG buffer and after the addition of 10 glycerol to 50% were frozen at -80 °C.

The TSAR-12 library thus formed had a working titer of $\sim 2 \times 10^{11}$ pfu/mL.

6.3. Characterization of the TSAR-9 and -12 Libraries

15 The inserted synthetic oligonucleotides for each of the TSAR libraries, described in Sections 6.1 and 6.2 above, had a potential coding complexity of 20^6 ($\sim 10^7$) and 20^{20} , respectively, and since $\sim 10^{14}$ molecules were used in each transformation experiment, each member of these TSAR 20 libraries should be unique. After plate amplification the library solution or stock has 10^4 copies of each member/mL.

It was observed that very few (<10%) of the inserted oligonucleotide sequences characterized so far in both of the libraries have exhibited deletions or insertions. This is 25 likely a reflection of the accuracy assembling the oligonucleotides under the conditions used and the fact that certain types of mutations (i.e., frame-shifts) would not be tolerated as pIII an essential protein for phage propagation.

In order to determine whether any coding bias existed in 30 the variant non-predicted peptides expressed by these libraries, perhaps due to biases imposed *in vitro* during synthesis of the oligonucleotides or *in vivo* during expression by the reproducing phage, inserts were sequenced as set forth below.

35

6.3.1. Characterization of TSAR-9 Library

Insert d synthetic ligonucleotid fragments of 23 rand mly chosen is lates wer examined fr m th TSAR-9 library. Individual plagu s w r us d to in culat e I ml f 2XYT broth containing *E. coli* (DH5aF') cells and the cultures 5 were allowed to grow overnight at 37°C with aeration. DNA was isolated from the culture supernatants according to Maniatis, *supra*. Twenty-three individual isolates were sequenced according to the method of Sanger (Proc. Natl. Acad. Sci. USA (1979) 74:5463-5467) using as a primer the 10 oligonucleotide 5'-AGCGTAACGATCTCCCG (SEQ ID NO. 99), which is 89 nucleotides downstream of the pIII gene cloning site of the m663 vector used to express the TSARS.

Nucleotide sequences and their encoded amino acid sequences were analyzed with the MacVector computer program 15 (IBI, New Haven, CT). The Microsoft EXCEL program was used to evaluate amino acid frequencies. Such analyses showed that the nucleotide codons coding for and hence most amino acids, occurred at the expected frequency in the TSAR-9 library of expressed proteins. The notable exceptions were 20 glutamine and tryptophan, which were over- and under-represented, respectively.

It is of interest to note the paucity of TAG stop codons in the inserts, i.e., only 2 of ~200 isolates characterized contained a TAG stop codon. About half [$1-(47/48)^{36}$] of the 25 phage inserts were expected to have at least one TAG codon in view of the assembly scheme used. However, most of the TAG-bearing phage appear to have been lost from the library, even though the bacterial host was *supE*. This may be a consequence of suppression being less than 100% effective.

30 The amino acids encoded by the inserted double stranded synthesized oligonucleotide sequences, excluding the fixed PG-encoding centers, were concatenated into a single sequence and the usage frequency determined for each amino acid using the Microsoft EXCEL program. These frequencies were compared 35 to that expected from the ass mbly schem of the oligonucleotides, and th div rg nce fr m exp cted values represented by the size of the bars above and below th

baseline. Chi square analysis was used to determine the significance of the deviations. The majority of amino acids were found to occur at the expected frequency, with the notable exceptions that glutamine and tryptophan were somewhat over- and under-represented, respectively. Thus, except for the invariant Pro-Gly, any position could have any amino acid; hence, the sequences are unpredicted or random.

6.3.2. Characterisation of TSAR-12 Library

Approximately 10 randomly chosen inserted oligonucleotides from the TSAR-12 library were examined by DNA sequencing as described above in Section 6.3.1. The isolates were chosen at random from the TSAR-12 library and prepared for sequencing, as were the TSAR-9 isolates. Analysis showed that except for the invariant Gly any position could have any amino acid; hence, the sequences are unpredicted or random.

6.4. Preparation of RSC Library

Referring now to Figure 3, two oligonucleotides were synthesized on an Applied Biosystems Model 380a machine with the sequence 5'-TGACGTCTCGAGTTGTNNKNNKNNKNNKNNKNNKNNKNNKTGTGGATCTAGAAGGATC-3' (SEQ ID NO:31) and 5'-GATCCTTCTAGATCC-3' (SEQ ID NO:32), where N is an equimolar ratio of deoxynucleotides A, C, G, and T, and K is an equimolar ratio of G and T. Fifty pmol of each oligonucleotide was incubated at 42 °C for 5 min, then 37 °C for 15 min, in 50 µL of Sequenase™ buffer (U.S. Biochemicals, Cleveland, OH) with 0.1 µg/µL acetylated BSA, and 10 mM DTT. After annealing, 10 units of Sequenase™ (U.S. Biochemicals) and 0.2 mM of each dNTP were added and incubated at 37 °C for 15 min. The sample was then heated at 65 °C for 2 hr, digested with 100 units of both Xho I and Xba I (New England BioLabs, Beverly, MA), phenol extracted, ethanol precipitated, and resolved on a 15% non-denaturing polyacrylamide gel. The assembled, digested fragment was gel purified prior to ligation. The vector, m663 (Fowlkes, D. t

al. Biotech. (1992) 13:422-427), was prepared by digestion with Xho I and Xba I, calf alkaline phosphatase (Boehringer Mannheim, Indianapolis, IN) treatment, phenol extracted, and purified by agarose gel electrophoresis. To ligate, 20 µg vector was combined with 0.2 µg insert in 3 mL with T4 DNA ligase (Boehringer Mannheim), according to the manufacturer. After removal of the protein and buffer by phenol extraction and ethanol precipitation, the ligated DNA was electroporated into XL1-Blue *E. coli* (Stratagene, San Diego, CA) and plated for eight hours at 37 °C. To recover the recombinant phage, the top agar was collected with a spatula, mixed with an equal volume of 100 mM NaCl, 10 mM MgCl₂, and 50 mM Tris-HCl (pH 7.5), and disrupted by two passes through an 18-gauge syringe needle. The bacterial cells were removed by centrifugation, and phage particles were collected by polyethylene glycol precipitation and stored at -70 °C in 25% glycerol. The library had 10⁸ total recombinants and a working titer of 6 x 10¹³ pfu/mL.

Members of the library were checked for inserts by the polymerase chain reaction (Saiki, et al. Science (1988) 239:487-491). Individual plaques on a petri plate were touched with a sterile toothpick and the tip was stirred into 2xYT with F⁺ *E. coli* bacteria and incubated overnight at 37 °C with aeration. Five microliters of the phage supernatant were then transferred to new tubes containing buffer (67 mM Tris-HCl, pH 8.8/10 mM β-mercaptoethanol/16.6 mM ammonium sulfate/6.7 mM EDTA/50 µg bovine serum albumin per mL), 0.1 mM deoxynucleotide triphosphates, and 1.25 units of Taq DNA polymerase (Boehringer Mannheim, Indianapolis, IN) with 100 pmoles of oligonucleotide primers. The primers flanked the cloning site in gene III of m663 (5'-TTCACCTCGAAAGCAAGCTG-3' (SEQ ID NO:100) and 5'-CCTCATAGTTAGCGTAACG-3' (SEQ ID NO:101)). The assembly reactions were incubated at 94 °C for 1 min, 56 °C for 2 min, and 72 °C for 3 min; this cycle was repeated 24 times. The reaction products were then resolved by electrophoresis on a NuSieve 2.0% agarose gel (FMC, Rockland, ME). Gels revealed

that for 20 plaques tested, all were recombinant and had single inserts of the expected size.

Based on the sample size of the library, it was anticipated that 100% of the recombinants had single inserts. However, all of the SH3-binding phage isolated from the R8C library had double-inserts. Such phage are presumed rare (i.e., <5%) within the library, yet because the SH3-binding peptide appears to need to be linear they were selected for by our screening methods. Most likely they were formed during the generation of the library; one scenario is that the inserts ligated together to form head-to-head dimers and that they were subsequently cloned into m663 DNA by ligation with the vector's *Xho I* sticky end and by illegitimate ligation with the vector's *Xba I* site (see, Figure 4).

15

6.5. Preparation Of Target-Coated Microtiter Wells

6.5.1. Preparation Of GST-SH3 Fusion Proteins

The preparation of Src-GST fusion protein was first described by Smith and Johnson, in Gene (1988) 67:31, the disclosure of which is incorporated by reference herein. Briefly, pGEX-derived (Pharmacia, Piscataway, NJ) constructs expressing GST fusion proteins containing the SH3 domains of Src, Grb2, Crk, Abl, or PLC γ were obtained from Dr. Channing Der (University of North Carolina at Chapel Hill); a construct expressing the SH3 domain of Yes was obtained from Dr. Marius Sudol (Rockefeller University). The use of the pGEX bacterial expression vector for the production of GST-SH3 fusion proteins is well-known to those in the art. See, e.g., Cicchetti, P. et al., in Science (1992) 257:803-806. Briefly, the coding region for a particular SH3 domain can be fused in-frame at the Bam HI site of pGEX-2T. Thus, fusion proteins were prepared as per the manufacturer's instructions, and quantified by Coomassie Blue staining of SDS-polyacrylamide gels. Microtiter wells were coated with 5-20 μ g GST-SH3 fusion protein in 100 mM NaHCO₃, pH 8.5, blocked with 100 mM NaHCO₃, (pH 8.5) 1% BSA, and washed. All washes consisted of five applications of

1XPBS, 0.1% Tween 20, 0.1% BSA (Buffer A). Where appropriate, the amount of protein bound to each well was quantified with an anti-GST antibody-based ELISA (Pharmacia, Piscataway, NJ), and with a GST-binding phage, isolated during the course of this work.

6.5.2. Coating of Microtiter Wells

Bacterially expressed Src SH3 glutathione-S-transferase (Src-GST) fusion protein was purified from bacterial lysates using glutathione agarose 4B (Pharmacia), according to the manufacturer's instructions. Bound Src-GST fusion protein was eluted from the glutathione agarose with 10 mM glutathione in PBS. Microtiter wells were then coated with Src-GST fusion protein (1-10 µg/well, in 50 mM NaHCO₃, pH 8.5) overnight at 4 °C. To block non-specific binding of phage, 100 µL 1% BSA in 100 mM NaHCO₃, pH 8.5, was added to each well and allowed to incubate at room temperature for 1 hour. The wells were then washed five times with 200 µL PBS, 0.1% Tween 20, 0.1% BSA (Buffer A).

6.6. Biopanning And Subsequent Characterisation Of Phage-Displayed Random Peptide Libraries With Src-GST Fusion Protein As Target Molecule

6.6.1. Isolation of Src SH3-Binding Phage

Library screens were performed as previously described. Kay, B.K., et al., in Gene (1993) 128:59-65. Briefly, 1 X 10¹¹ pfu TSAR 9, TSAR 12, or R8C phage in Buffer A were incubated in a Src SH3-GST-coated well for 2 hours. The wells were washed, and bound phage were eluted with 100 µL 50 mM glycine-HCl (pH 2.2), transferred to a new well, and neutralized with 100 mL 200 mM NaHPO₄ (pH 7.0). Recovered phage were used to infect 1 x 10⁹ DH5αF' *E. coli* cells in 20 mL 2xYT; the infected cells were grown overnight, resulting in a 1000- to 10,000-fold amplification of phage titer. Amplified phage were panned twice more, as above, excepting the amplification step. Binding phage recovered after the third round of panning were plated at a low density on a lawn of DH5αF' *E. coli* cells to yield

is lated plaqu s f r cl nal analysis. Isolated plaques were
us d t produc small cultures fr m which phage stocks and
DNA were r cover d for phag binding experiments and dide xy
sequencing (Sanger, F., et al., in Proc. Natl. Acad. Sci. USA
5 (1977) 74:5463-5467), respectively. Clones were confirmed as
binding the SH3 domain by applying equal titers of phage to
wells containing Src SH3-GST or GST alone, and titering the
number of eluted particles from each well, or detecting bound
phage with an anti-phage antibody-based ELISA (Pharmacia).

10 Indeed, the ability of isolated phage clones to bind to
several SH3 domains derived from a variety of different
proteins can be investigated by the manner described above.
GST-SH3 fusion proteins containing SH3 domains from a variety
of different proteins are bound to microliter wells. An
15 aliquot of the aforementioned phage stocks (50 μ L) is
introduced into wells containing the different GST-SH3 fusion
proteins. After room temperature incubation for 1-2 hours,
the liquid contents of the microtiter plates are removed, and
the wells are washed 5 times with 200 μ L Buffer A. Bound
20 phage are eluted with 100 μ L 50 mM glycine (pH 2.2),
transferred to a new well, and neutralized with 100 μ L 200 mM
NaHP0₄ (pH 7.0). The phage are diluted 10^3 - to 10^6 -fold, and
aliquots are plated onto lawns of DH5 α F' E. coli cells to
establish the number of plaque forming units in the output
25 sample. From these experiments, the relative specificity of
different Src SH3 binding clones for SH3 domains derived from
other proteins is determined.

6.6.2. Phage ELISA and Nucleotide Sequencing

30 To evaluate the binding of isolates to
various targets proteins, enzyme-linked-immuno-assays (ELISA)
were also performed. Bacterial cultures were infected with
phage isolates and cultured overnight in 2XYT at 37 °C. The
cells were spun down and 25 mL of supernatant was added to
35 microtiter plate w lls c ated with 50 mL of protein (1 mg/mL
in 100 mM NaHCO₃, pH 8.4; overnight at 4 °C or f r a few hours
at room temperature) and blocked (1 mg/mL BSA in 100 mM

NaHCO₃, pH 8.4; for about one hour). The phages are incubated in the wells with 25 mL of PBS-0.1% Tween 20 at RT for 2 hr. The wells are then washed multiple times over 30 minutes. To each well is added 50 µL of polyclonal anti-phage antibody conjugated to horseradish peroxidase. The antibody is diluted 1:3000 in BSA-PBS-Tween 20; it was obtained from Pharmacia (Piscataway, NJ; catalog number 27-9402-01). After 30 minutes, the wells are washed again with BSA-PBS-Tween 20 for 20 minutes. Finally, 100 µL of ABTS reagent (Pharmacia, with H₂O₂) are added to each well for the development of color. Plates are read with a plate reader (Molecular Devices, Menlo Park, CA) at 405 nm wavelength.

The nucleotide sequence of the relevant segments of the Src SH3 binding clones (or phage clones that bind to SH3 domains of other proteins) were sequenced using standard methods. Sanger, F., et al., in Proc. Natl. Acad. Sci. USA (1977) 74:5463-5467. The oligo primer 5'-AGCGTAACGATCTAAA-3' (SEQ ID NO:102) was used, which is 89 nucleotides downstream of the gene III cloning site of M13 m666. The nucleotide sequences were analyzed with the MacVector computer program (IBI, New Haven, CT, USA). From this nucleotide sequence information the primary sequence of each Src SH3 binding peptide was deduced. The corresponding synthetic peptides were then prepared by techniques well known in the art with or without flanking sequences. Indeed, these synthetic peptides have been shown to bind to SH3 domain targets, with those possessing the phage flanking amino acid residues exhibiting greater binding affinity.

30 6.7 In Vitro Peptide Binding Assays

Peptides were obtained from Research Genetics (Birmingham, AL), Chiron Mimotopes (Victoria, Australia), or synthesized by conventional techniques by Dr. J. Mark Carter of Cytogen Corporation (Princeton, NJ). Peptide purity was assessed by HPLC and/or mass spectrometry. Biotinylated peptides were synthesized with either a KSGSG (SEQ ID NO:103) or a GSGS (SEQ ID NO:104) peptide linker (a spacer) between

the biotin and the N-terminus of the peptide. Binding experiments were performed as above, excepting the use of 10 μ M peptide instead of phage. Bound biotinylated peptide was detected with streptavidin conjugated to alkaline phosphatase (Sigma Chemical Co., St. Louis, MO). After one hour incubation period at room temperature, the wells were washed, and a solution of 3 mM p-nitrophenyl-phosphate (US Biochemicals, Cleveland, OH) in 50 mM NaCO₃ (pH 9.8), and 50 mM MgCl₂ was added and color allowed to develop. Signals were read with an ELISA plate reader (Molecular Devices, Menlo Park, CA) at 405 nm wavelength. Binding experiments were performed in triplicate. The results are presented in Figures 7 and 8.

15 **6.8. Peptide Competition of GST-SH3 Affinity Precipitations of Cell Lysates**

Labeled proteins are prepared by incubating a culture of HeLa cells overnight with ≥ 100 μ Ci/mL ³⁵S-methionine. The cells are then washed and lysed with mild detergent. This mixture of radioactive proteins is incubated with Src-GST fusion protein that has been immobilized on glutathione-linked Sepharose beads (Pharmacia, Piscataway, NJ). After several hours of tumbling, the beads are pelleted gently by low-speed centrifugation, and the supernatant is discarded. The beads are then resuspended into a slurry in PBS-0.1% Tween 20, pelleted, and washed several additional times. Finally, a 2% SDS solution is added to the sample, which is then boiled at 100 °C for 3 minutes. Afterward, the sample is centrifuged, and the supernatant loaded on a 10% polyacrylamide SDS gel for electrophoresis. After the proteins have been resolved, the gel is fixed, dried down, and exposed to X-ray film for autoradiography or phosphor plates for scanning by a Molecular Dynamics PhosphorImager.

The ability of Src SH3 to bind certain ³⁵S-labeled proteins is examined for compatibility with exogenous peptides. Synthetic peptides corresponding to phage-displayed inserts and motifs are added at the time that the

lysate is incubated with the Src-GST fusion protein immobilized on glutathione-linked sepharose beads. The SH3 binding peptide blocks binding of all or some of the labeled proteins while negative control peptides (unrelated peptide sequences) do not. The amount of competition is quantified and correlated with the amount of added SH3-domain binding peptides.

Alternatively, NIH 3T3 cells were grown in Dulbecco's Modified Eagle Medium (DME) + 10% fetal calf serum (FCS) + 80 $\mu\text{Ci/mL}$ Tran³⁵S-label (ICN), washed with PBS, lysed in RIPA buffer, and pelleted. Supernatant from 1.5×10^6 cells was precleared with 100 μg glutathione-agarose-immobilized GST. The supernatant was then incubated with 10 μg glutathione-agarose-immobilized GST-SH3 fusion protein with or without added test peptide in a final volume of 250 μL . Pelleted beads were washed with 1 mL each of RIPA, RIPA + 1% deoxycholate + 0.1% SDS, and PBS, resuspended in 50 μL SDS-PAGE sample buffer, boiled, and subjected to SDS-PAGE (7.5%). Labeled proteins were detected by phosphorimaging (Molecular Dynamics). The results are presented in Figure 9.

6.9. Peptide Competition of GST-SH3 Affinity Precipitations of PI-3' Kinase From Cell Lysates

It is possible to follow the precipitation of PI-3' Kinase by Src from cell lysates in the presence or absence of SH3-binding peptides. HeLa cells are lysed with detergent and the protein mixtures are incubated for several hours with the Src-GST fusion protein immobilized on glutathione-linked Sepharose beads. After several hours of tumbling, the beads are pelleted gently by low-speed centrifugation and the supernatant is discarded. The beads are then resuspended into a slurry in PBS-0.1% Tween 20, pelleted, and washed several additional times. Finally, an SDS solution is added to the sample, which is then boiled at 100 °C for 3 minutes. Subsequently, the sample is centrifuged, and the supernatant is loaded on a 10% polyacrylamide SDS gel for electrophoresis. After the proteins have been resolved, the

g 1 is blotted to nitrocellulose or nylon (i.e., western blot). The filter is then probed with a PI-3' Kinase antibody (monoclonal and polyclonal antibodies are available from Upstate Biotechnology Incorporated, Lake Placid, NY), and an enzyme-linked secondary antibody. The amount of PI-3' Kinase is then quantitated.

The ability of Src SH3 to bind PI-3' Kinase is examined for competitiveness with exogenous peptides. Synthetic peptides corresponding to phage-displayed inserts and motifs are added at the time that the lysate is incubated with the Src-GST fusion protein that has been immobilized on glutathione-linked sepharose beads. Ten-fold and one hundred-fold molar excess of peptides are used relative to SH3 proteins. The SH3 binding peptides block binding of the PI-3' Kinase as detected on western blots while negative control peptides (unrelated peptide sequences) do not. The amount of competition is quantified and correlated with the amount of added SH3-domain binding peptides.

20 6.10. **In Vivo Association Of SH3-Binding Peptides With SH3-Domains Of Proteins**

To demonstrate association of the SH3-binding peptides with SH3-domains of proteins inside cells, the SH3-binding peptides are tagged and localized in cells. For example, Bar-Sagi et al., in Cell (1993) 74:83-91, have shown that SH3-binding proteins localize to the cytoskeleton when expressed in cells. Thus, the SH3 domain-binding peptides of the present invention can serve as cellular targeting signals (e.g., to the cytoskeleton). Accordingly, the peptides are tagged with biotin and, subsequently, injected into cells. Alternatively, one can transfect into cells a recombinant plasmid that expresses a fusion protein comprising of the SH3-binding peptide and the green fluorescent protein (GFP, Chalfie et al., in Science (1994) 263:802-805). The location of the biotinylated peptide or the GFP fusion protein is then assayed with FITC-labeled streptavidin in paraformaldehyde-fixed cells or by direct

fluorescence in living cells, respectively. Localization of the SH3-binding peptides to the cytoskeleton demonstrates that the SH3-binding peptides can bind SH3-domain proteins *in vivo*. In addition, focal adhesions, which are rich in Src, are also sites of potential subcellular localization of SH3-binding peptides.

Thus, NIH 3T3 fibroblasts were cultured *in vitro* on glass coverslips coated with fibronectin. After two days of growth at 37 °C, the cells were fixed for one hour at room temperature in the presence of 2% paraformaldehyde (pH 7.5). The coverslips were washed with PBS-0.1% Tween 20 several times to remove the fixative. Next, the coverslips were dipped into acetone (chilled at -20 °C) for approximately 20 seconds and allowed to air-dry. The coverslips were washed again with PBS-0.1% Tween 20, containing BSA (1 mg/mL), and incubated for 2 hours at room temperature with different biotinylated peptides in PBS-0.1% Tween 20. The coverslips were washed and then incubated with 1 mg/mL streptavidin-Cy3 (Jackson ImmunoResearch Co., West Grove, PA) for 1 hour at room temperature. Finally, the coverslips were washed in PBS-0.1% Tween 20, mounted in a glycerol solution on a glass slide, and viewed with a Nikon Optiphot epifluorescence microscope and a 60x oil immersion lens.

The results are presented in Figure 11, in which panel A displays cells stained with the conjugate biotin-spacer-VLKRPLPIPPVTR (SEQ ID NO:64); panel B exhibits cells stained with the conjugate, biotin-spacer-GILAPPVPPRNTR (SEQ ID NO:63); panel C shows cells stained with the long consensus peptide, biotin-spacer-RSTPRPLPPLPTTR (SEQ ID NO:67); and panel D shows cells stained with the proline-rich vinculin peptide conjugate, biotin-spacer-LAPPKPPLPEGEV (SEQ ID NO:70). The "spacer" sequence is KSGSG (SEQ ID NO:103). As shown in Figure 11, the panels in which SH3 domain-binding peptides were used present a bright display of fluorescence activity that is in sharp contrast to the relatively "dark" features of panel D (non-SH3 domain binding vinculin segment). These results demonstrate further the ability of

the SH3 domain-binding peptides of the present invention to localize to protein targets (e.g., Src and Src-related proteins) within cells and provide an image thereof.

5 6.11. **In Vivo Modulation Of Src In Oocytes With SH3-Binding Peptides**

When *Xenopus laevis* oocytes are injected with mRNA encoding deregulated Src, there are dramatic cytological and biochemical changes in the oocyte (Unger, T.F. and Steele, R.E., in Mol. Cell. Biol. (1992) 12:5485-5498). The
10 applicants have obtained the plasmid for generating Src mRNA, which is available from Dr. Robert Steele (University of California at Irvine). Synthetic SH3-binding peptides are injected into oocytes that have been previously injected with
15 Src mRNA. The state of the cytoskeleton is inspected visually by observing the arrangement of cortical pigment granules under a dissecting microscope. The state of phosphorylation of several proteins is examined by western blotting with an anti-phosphotyrosine monoclonal antibody
20 (4G10; Upstate Biotechnology Incorporated), as described in Unger and Steele, above.

 6.12. **Progesterone-induced *X. laevis* Oocyte Maturation**

Segments of adult ovary were removed
25 surgically and incubated in 0.1% collagenase type D (Boehringer Mannheim, Indianapolis, IN) in Ca²⁺-free OR2 (82.5 mM NaCl, 2.5 mM KCl, 1.0 mM MgCl₂, 1.0 mM Na₂HPO₄, 5.0 mM HEPES, and 3.8 mM NaOH, pH 7.6). Oocytes were then washed 3-
30 5 times with OR2 containing 1.0 mM CaCl₂ and allowed to recover in OR2 overnight at 18 °C. Stage VI oocytes were injected with 40 nL of 100 mM peptide or water. After injection, the oocytes were placed in OR2 with 2 mg/mL progesterone (Sigma, St Louis, MO) and incubated at 20 °C. Oocytes were scored at hourly time points for germinal
35 vesicle breakdown (GVBD).

Figure 10 presents the results of this experiment. As shown by the graph, oocytes injected with the SH3 domain-binding peptide VLKRPLPIPPVTR (SEQ ID NO:64) exhibit a faster rate of progesterone-induced germinal vesicle breakdown relative to oocytes that had been injected with water or with the proline-rich vinculin peptide, LAPPKPPLPEGEV (SEQ ID NO:70). These results parallel those obtained by Unger and Steele, *supra*, who observed a gross alteration in the cortex of oocytes that had been injected with RNA encoding a deregulated Src variant ("active" Src) versus those injected with RNA encoding the wild-type Src ("cellular" Src). Also, as shown in Figure 3B of the Unger and Steele article, oocytes injected with deregulated or active Src RNA matured at a faster rate than oocytes injected with water or wild-type Src RNA.

The present results obtained with Src SH3 domain-binding peptides suggest that these peptides modulate the biochemical activity of "cellular" Src; in particular, it is proposed that at least some of the Src SH3 domain-binding peptides of the present invention upregulate the biochemical activity of "cellular" Src, which may be downregulated or inhibited in its normal state. Hence, the administration of the SH3 domain-binding peptides of the present invention can constitute a novel method of modulating the activity of Src or Src-related proteins. Specifically, certain of these peptides are able to activate Src-family proteins.

6.13. In Vivo Antagonism Of Src In Src Transformed Cells With SH3-Binding Peptides

The coding regions for SH3-binding peptides are cloned into vectors that direct their expression in animal cells. A bipartite gene is constructed, encoding a protein with c-myc epitope and SH3-binding peptide, which is transcribed from a strong constitutive promoter (e.g., SV40, CMV, HSV TK, calmodulin). The vector is introduced into either normal or Src-transformed cells via transfection (e.g., electroporation, calcium phosphate, liposomes, DEAE

d xtran). Transfected cells express the bipartite gene transiently in culture. To create stable transformed cell lines, the vector carries a selectable marker (e.g., neomycin resistance) or transfection is performed in the presence of excess plasmid carrying a selectable marker (e.g., neomycin resistance) and cells selected for the marker. Transfected cells are stained by immunofluorescence to detect expression of the bipartite protein. The hybridoma 9E10 secretes a monoclonal antibody that is highly specific for the c-myc epitope (EQKLISEEDLN [SEQ ID NO:105]; see, Evan, G.A. et al., in Mol. Cell. Biol. (1985) 5:3610-3616). This antibody is used in immunofluorescence experiments to demonstrate that the bipartite protein is expressed inside the cells, and in some cases, localized to subcellular structures enriched in SH3 domain bearing proteins.

There are several controls used in these experiments. First, cells are transfected with vectors that do not have the SH3-binding peptide coding region. Second, normal (non-transformed) cells are transfected. Third, cells transformed by oncogenes other than Src are used in the transfection experiments. Fourth, cells are stained with other monoclonal antibodies that do not recognize the c-myc epitope.

Transfected cells are examined for any changes in cell shape, behavior, and metabolism as a consequence of expressing the SH3 binding peptides. Cell shape is examined by phase contrast microscope at several times after transfection; in particular, the flatness of the cells, their adhesion to the substrate, and the degree of cell ruffling are monitored. Cell division rates, cell migration, and contact inhibition are also observed over time. Finally, the amount of phosphorylated tyrosine in transfected cells is quantitated by phosphoaminoacid analysis and with an anti-phosphotyrosine monoclonal antibody (4G10; Upstate Biotechnology Incorporated) in western blotting experiments.

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6.14 Preparation of PXXP Biased Peptide Libraries

The preparation and characterization of preferred phage-displayed random peptide libraries have been described above in Sections 6.1 - 6.4.

- 5 Using procedures similar to those described in these sections, oligonucleotide inserts were constructed according to the schematic provided in FIG. 12. The inserts were then cloned into the mBAX vector, and the biased peptide libraries were expressed as described previously.
- 10 The mBAX vector was created in the Kay Laboratory by generating cloning sites in gene III of the M13mp18 vector (Messing, J. (1991). Cloning in M13 phage or how to use biology at its best. Gene 100, 3-12) in the manner of Fowlkes et al. (1992) (Biotechniques 13, 422-427). The mBAX
- 15 vector displays a peptide sequence at the N-terminus of the mature pIII protein that encodes the epitope for the mouse monoclonal antibody 7E11 (see, FIG. 13); it includes the stop codon TAG in the coding region, which is suppressed in *E. coli* carrying suppressor tRNA gene mutations known as *supE* or
- 20 *supF*. There are no other stop codons in the mBAX genome. The mBAX vector also carries a segment of the alpha fragment of β -galactosidase; bacterial cells expressing the omega fragment of β -galactosidase convert the clear XGal substrate into an insoluble blue precipitate. The plaques appear blue.
- 25 Recombinant mBAX molecules can be distinguished easily from non-recombinant molecules due to the TAG codon in the *Xho*I - *Xba*I segment in gene III of mBAX. When recombinants are generated by replacing the *Xho*I - *Xba*I fragment with oligonucleotides encoding random peptides, the recombinants
- 30 can be grown in bacteria with (i.e., DH5 α F') or without (i.e., JS5) suppressor tRNA mutant genes. On the other hand, the non-recombinant mBAX molecules fail to produce plaques on bacterial lawns where the bacteria (i.e., JS5) lack such suppressor genes. This is because in JS5, the TAG codon
- 35 serves as a stop codon to yield a truncated pIII molecule during translation; since pIII is an essential protein

component of viable M13 viral particles, no plaques will form.

6.14.1 Discussion

The use of second generation or biased peptide libraries, which fix all or part of the RPLPPLP consensus motif for SH3 binding peptides and randomize flanking residues, has defined additional sequence residues exhibiting selective SH3 binding.

Tables 1-5, below, list the relevant amino acid sequences obtained from the biased peptide library for each set of SH3 domain binding peptides. The underscored amino acid residues indicate the fixed positions. Also, indicated for each set of new binders is a "consensus" sequence, which seeks to include the additional features gleaned from the new binding peptides. The symbol " ϕ " represents a hydrophobic residue.

TABLE 1 CORTACTIN SH3-BINDING PEPTIDES

		SEQ. ID NO.
20	PXXP.CORT.M1/2/3.PP	SSLLGPPVPPKPQTLFSFSR
	PXXP.CORT.M4.PP	SRLGEFSKPPIPQKPTWMSR
	PXXP.CORT.N2.PP	SRTERPPLPQRPDWLSYSSR
	PXXP.CORT.N3.PP.INC	SREPDWLCPNCP LL LRSDSR
25	PXXP.CORT.01/2/3.PP	SSSSHNSRPPLP E KPSWLSR
	PXXP.CORT.04.PP	SRLTPQSKPPLPPKPSAVSR
	CONSENSUS	KPP ϕ PxKPxW R
		113

30

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TABLE 2

NCK SH3-BINDING PEPTIDES

		SEQ. ID NO.
5	PXXP.NCK.Q1/4.PP	<u>SSLGVGWKPLPPMRTASLSR</u> 114
	PXXP.NCK.Q2/3.PP.INC	<u>SSVGFADRPRLRVESLSR</u> 115
	PXXP.NCK.R1.PP.INC	<u>SSAGILRPPEKPKRSFSLSR</u> 116
	PXXP.NCK.R2.PP	<u>SSPYTGDVPIPLRGASLSR</u> 117
	PXXP.NCK.R3.PP	<u>SSLMGSWPPVPLRSDSLSR</u> 118
10	PXXP.NCK.R4.PP	<u>SSIGEDTPSPPTRRASLSR</u> 119
	PXXP.NCK.S1/4.PP	<u>SRSLSEVSPKPPIRSVSLSR</u> 120
	PXXP.NCK.S2.PP.INC	<u>SSVSEGYSPPLPPRSTLSR</u> 121
	PXXP.NCK.S3.PP	<u>SSSFTLAAPTPTPTRLSSLRSR</u> 122
	PXXP.NCK.T1.PP	<u>SSPPYELPPRPPNRTVSLSR</u> 123
15	PXXP.NCK.T2.PP	<u>SRVVDGLAPPPVRLSSLSR</u> 124
	PXXP.NCK.T3.PP.INC	<u>SSLGYSGAPVPPHRxSSLSR</u> 125
	PXXP.NCK.T4.PP	<u>SSISDYSRPPPPVRTLSLSR</u> 126
	CONSENSUS	φxxxxxxPxPPφRSxSL T127
20		

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30

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TABLE 3 ABL SH3 BINDING PEPTIDES

		SEQ. ID NO.	
	PXXP.ABL.G1/2.PP	SRGPRWSPPPVPLPTSLDSR	128
5	PXXP.ABL.G3/4.PP	SSPPDYAAPAISSLWVDSR	129
	PXXP.ABL.H1/3/4.PP	SSPPHWAPPAPPAMSPPI SR	130
	PXXP.ABL.H2.PP.INC	SSDRCWECPPWPAGGQRGSR	131
	PXXP.ABL.I1/2/3.PP	SSPPKFSPPPPPYWQLHASR	132
10	PXXP.ABL.I4.PP	SSPPSFAPPAAPPRHSFGSR	133
	PXXP.ABL.J1.PP	SSAPKKPAPPVPMMAHVMSR	134
	PXXP.ABL.J2.PP.INC	SSPTYPPPPPPDTAKGASR	135
	PXXP.ABL.J3.PP.INC	SSPPXXXPPPIPNSPQVLSR	136
	PXXP.ABL.J4.PP	SSPPTWTTPKPPGQGVVFSR	137
15	PXXP.ABL.L1.PP	SSAPTWSPPALPNVAKYKSR	138
	PXXP.ABL.L2/3.PP	SSIKGPRFPVPPVPLNGVSR	139
	PXXP.ABL.L4.PP	SSPPAWSPPHRPVAFGSTSR	140
	CONSENSUS	PPxWxPPPøP	141

20 TABLE 4 PLCG SH3-BINDING PEPTIDES

		SEQ. ID NO.
	PXXP.PLCG.P1.PP	<u>SSMKVHNFPPLPSYETSR</u> 142
	PXXP.PLCG.P2.PP	<u>SRVPPLVAPRPPSTLNSLSR</u> 143
25	PXXP.PLCG.PE.PP.INC	<u>SSLYWQHGPDPVGAPQLSR</u> 144
	PXXP.PLCG.P4.PP	<u>SSHPLNSWPGGPFRHNLSSR</u> 145

30

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TABLE 5 SRC SH3-BINDING PEPTIDES

		SEQ. ID NO.
5	PXXP.SRC.A1.PP	<u>SSRALVRPLPPVPGTSLSR</u> 146
	PXXP.SRC.A2.PP	<u>SSFRALPLPPTPDNPFAGSR</u> 147
	PXXP.SRC.A3.PP	<u>SRDAPGSLPFRPLPPVPTSR</u> 148
	PXXP.SRC.A4.PP	<u>SSISQRALPPLPLMSDPASR</u> 149
10	PXXP.SRC.B1.PP	<u>SSPAYRPLRLPDLSVIYSR</u> 150
	PXXP.SRC.B2/3/PP	<u>SSFINRRLPALPPDNSLLSR</u> 151
	PXXP.SRC.B4.PP	<u>SRLTGRPLPALPPPFSDFSR</u> 152
	PXXP.SRC.C1.PP	<u>SRMKDRVLPPIPTVESAVSR</u> 153
	PXXP.SRC.C2.PP.INC	<u>SSLYSAIAPDPPPRNSSSSR</u> 154
15	PXXP.SRC.C3.PP	<u>SSLASRPLPLLNSAPGQSR</u> 155
	PXXP.SRC.D1.PP	<u>SSLTSRPLPDIPVRPSKSSR</u> 156
	PXXP.SRC.D2.PP.INC	<u>SSLKWRALPPLPETDTPYSR</u> 157
	PXXP.SRC.D3.PP	<u>SSNTNRLPPPTPDGLDVRSR</u> 158
20	PXXP.SRC.D4.PP	<u>SSLQSRPLPLPPQSSYPISR</u> 159
	CONSENSUS	RPLPLP 160

It should be apparent to one of ordinary skill that many other embodiments of the present invention can be contemplated beyond the preferred embodiments described above but which other embodiments nevertheless fall within the scope and spirit of the present invention. Hence, the present invention should not be construed to be limited to the preferred embodiments described herein, which serve only to illustrate the present invention, but only by the claims that follow.

Also, numerous references are cited throughout the specification. The complete disclosures of these references are incorporated by reference herein.

SEQUENCE LISTING

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- (ii) TITLE OF INVENTION: Src SH3 BINDING PEPTIDES AND METHODS OF ISOLATING AND USING SAME
- (iii) NUMBER OF SEQUENCES: 106
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- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
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(C) TELEX: 66141 PENNIE
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "hydrophobic residue (such as Pro or Leu)"
- (xi) SEQUENCE DESCRIPTION: SEQ ID N :1:
- | | | | | | | | | | |
|-----|----|-----|-----|-----|-----|----|-----|-----|-----|
| Xaa | Pr | Xaa | Xaa | Pro | Pro | Pr | Xaa | Xaa | Pro |
| 1 | | | | 5 | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
- 5 (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 1..3
 (D) OTHER INFORMATION: /note= "Xaa = any residue other than Cys"
- 10 (ix) FEATURE:
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 (B) LOCATION: 6
 (D) OTHER INFORMATION: /note= "X = any residue other than Cys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8..9
 (D) OTHER INFORMATION: /note= "X = any residue other than Cys"
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 Xaa Xaa Xaa Pro Pro Xaa Pro Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:3:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "X tends to be hydrophobic"
- 25 (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 8..9
 (D) OTHER INFORMATION: /note= "X tends to be hydrophobic"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
 Arg Xaa Leu Pro Pro Arg Pro Xaa Xaa
 1 5
- 30

(2) INFORMATION FOR SEQ ID NO:4:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Lys Leu Pro Pr Arg Pro Arg Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:5:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10

Val Pro Pro Pro Val Pro Pro Arg Arg Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:6:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "tends to be Pro"

20

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 3
 (D) OTHER INFORMATION: /note= "hydrophobic residue"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "tends to be Pro"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Xaa Xaa Pro Xaa Xaa Pro
 1 5

30 (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

35

(ix) FEATURE:

- (A) NAME/KEY: Modified-sit
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "X = any residue other than Cys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 8..9

(D) OTHER INFORMATION: /n t = "X = any r sidue other than Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5

Arg Xaa Leu Pro Pro Arg Pro Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 9

15

(D) OTHER INFORMATION: /note= "hydrophobic residue"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Xaa Leu Pro Pro Leu Pro Arg Phe
1 5

(2) INFORMATION FOR SEQ ID NO:9:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

25

Arg Pro Leu Pro Pro Leu Pro
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "any residue other than Cys"

35

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5..6

(D) OTHER INFORMATION: /n t = "any hydr phobic residue"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 9

(D) OTHER INFORMATION: /not = "any hydrophilic residu
except Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5

Arg Xaa Leu Pro Xaa Xaa Pro Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Pro Leu Pro Pro Leu Pro Thr Ser
1 5

15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Xaa Xaa Xaa Xaa
1

25

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

30

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Xaa Xaa Xaa Xaa Xaa
1 5

35 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amin acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5 Xaa Xaa Xaa Xaa
1

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 1..3
(D) OTHER INFORMATION: /note= "any residue other than Cys"

15 (ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "any residue other than Cys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 8..9
(D) OTHER INFORMATION: /note= "any hydrophobic residue"

20 (ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 11..13
(D) OTHER INFORMATION: /note= "any residue other than Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

25 Xaa Xaa Xaa Arg Xaa Leu Pro Xaa Xaa Pro Xaa Xaa Xaa
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
35 Xaa Xaa Xaa Xaa Pr Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Arg

35

40

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

5 GGCTCGAGNN NBNNBNNBNN BNNBNNBNNB NNBNNBNNBN NBNNBNNBNN BNNBNNBNNB 60
10 NNBCCAGGT 69

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

15 GGTCCANNVN NVNNVNNVNN VNNVNNVNNV NVNNVNNVN NVNNVNNVNN VNNVNNVNNV 60
20 AGATCTGG 68

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

25 TCGAGNNBNB NBNNBNNBNN BNNBNNBNNB NNBNNBNNBN NBNNBNNBNN BNNBNNBNNB 60
30 CCAGGT 66

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

35

GGTCCANNVN NVNNVNNVNN VNNVNNVNNV NNVNNVNNVN NVNNVNNVNN VNNVNNVNNV

60

AGATC

65

(2) INFORMATION FOR SEQ ID NO:21:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

- 10 (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "Arg or Ser"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

15 Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Pro Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Arg Pro Ser Arg Thr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:22:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 Ser His Ser Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Arg Pro Ser Arg
 35 40 45
 30 Thr

(2) INFORMATION FOR SEQ ID NO:23:

- 3 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Ser or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /note= "Ser, Arg, Gly, Cys or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Val, Ala, Asp, Glu or Gly"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

20 TTTTGTGCGAC NNNBNNBNNB NNBNNBNNBN NBNNBNNBNN BNGCGGTG 48

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCCACNVNN VNNVNNVNNV NNVNNVNNVN NVNNVNNVTG ATCATTTT 48

30 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

35 CGCCACNVNN VNNVNNVNNV NNVNNVNNVN NVNNVNNVTG ATC 43

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCGACNNNNBN NBNNNNNNNBN BNNBNNNBNNB NNBNNNBNGCG GTG

43

(2) INFORMATION FOR SEQ ID NO:28:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE:
- 15 (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "Ser or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "Ser, Arg, Gly, Cys or Trp"
- 20 (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 15
 (D) OTHER INFORMATION: /note= "Val, Ala, Asp, Glu or Gly"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
- 25 Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Pro Ser Arg Thr
 20 25 30

(2) INFORMATION FOR SEQ ID NO:29:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 5
 (D) OTHER INFORMATION: /note= "Ser r Thr"
- 35 (ix) FEATURE:
 (A) NAME/KEY: Modified-site

- (B) LOCATION: 16
 (D) OTHER INFORMATION: /note = "Ser, Arg, Gly, Cys or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 18
 (D) OTHER INFORMATION: /note = "Val, Ala, Asp, Glu or Gly"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ser His Ser Ser Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Arg Pro Ser
 20 25 30

10

Arg Thr

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

20

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

30

TGACGTCTCG AGTTGTNNKN NKNNKNNKNN KNNKNNKNNK TGTGGATCTA GAAGGATC

58

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CCTAGATCTT CCTAG

15

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TCGAGTTGTN NKNKNKNKN NKNKNKNKNK NNKTGTGGAT
 10

40

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CAACANNMNN MNNMNNMNNM NNNMNNMNNMA CACCTAGATC
 15

40

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ser Ser Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Gly Ser Arg Pro
 1 5 10 15

Ser Arg Thr

30 (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Ser Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Gly Ser Arg Ser
 1 5 10 15

Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Thr Arg
20 25

(2) INFORMATION FOR SEQ ID NO:37:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

10 TCGAGTTGTN NKNNKNNKNN KNNKNNKNNK NNKTGTGGAT CTAGATCCAC AVNNVNNVNN 60
 VNNVNNVNNV NNVNNACAAC 80

(2) INFORMATION FOR SEQ ID NO:38:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20 Ser Ser Phe Asp Gln Gln Asp Trp Asp Tyr Ser Ile Ala Glu Lys Met
 1 5 10 15
 His Pro Ile Arg Pro Gly Phe Arg Glu Leu Pro Pro Leu Pro Pro Ser
 20 25 30
 Arg Ala Ser Phe Gly Gly Gly Ala Ser Arg Pro Ser Arg
 35 40 45

25 (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Thr Asn Val Trp Val Thr Gly Ser Val Ile Ala Arg Gly Ala Gln
 1 5 10 15
 Ser Arg Pro Leu Pro Ile Pro Pro Glu Thr Arg Pro Ser Arg
 20 25 30

35 (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amin acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

5 Ser Thr Ala Pro Trp Gly Leu Arg Val Ala His Glu Gly Gly Val Leu
1 5 10 15
Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg Pro Ser Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:41:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

15 Ser Ser Ser Gly Tyr Val Val Pro Lys Arg Leu Gly Asp Met Arg Glu
1 5 10 15
Tyr Asn Ala His Pro Gly Leu His Val Pro Pro Asn Ser Pro Leu Pro
20 25 30
Pro Leu Pro Thr His Leu Gln Ser Ser Arg Pro Ser Arg
35 40 45

20 (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Ser Arg Gly Glu Gly Asn Asn Ile Ile Ser Ser Arg Pro Phe Leu
1 5 10 15
Ser Asn Ser Asp Pro Gly Val Ser Asn Lys Leu Thr Gly Arg Gly Pro
20 25 30
Leu Pro Pro Leu Pro Asn Asp Ser Arg Pro Ser Arg
30 35 40

(2) INFORMATION FOR SEQ ID NO:43:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Thr Ala Val S r Ph Arg Phe Met Pr Gly Gly Gly Gly Ala Ph
 1 5 10 15
 Tyr Ser Thr Arg Pro Val Pro Pr Ile Thr Arg Pro Ser Arg Thr
 20 25 30

5 (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Thr Ala His Ser Leu Trp Asp Trp Gly Thr Phe Ser Gly Val Ser
 1 5 10 15
 His Lys Ser Arg Leu Pro Pro Leu Pro Thr Arg Pro Ser Arg Thr
 20 25 30

15

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Pro Gly Tyr Ala Arg Ile Val Ser Tyr Arg Phe Arg Ala Leu Pro Ser
 1 5 10 15
 Pro Pro Ser Ala Ser Arg Pro Ser Arg
 20 25

25

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ser Thr Asn Asp Val Asp Trp Met His Met Trp Asn Ser Gly Gly Pro
 1 5 10 15
 His Arg Arg Leu Pro Pro Thr Pro Ala Thr Arg Pro Ser Arg
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amin acids
 (B) TYPE: amin acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Ser Asp Asn Trp Ala Arg Arg Val His Ala Ser Glu Leu Ile Tyr
 1 5 10 15
 Thr Asp Leu Ser Pro Gly Ile Leu Leu Ala Gln Arg Gln Leu Pro Pro
 20 25 30
 Thr Pro Gly Arg Asp Pro Ser His Ser Arg Pro Ser Arg
 35 40 45

10

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Ser Glu Ser Pro Leu Met Tyr Asn Arg Val Gly Ala Leu Gln Ser
 1 5 10 15
 Leu Thr Ser Val Pro Gly Ser Met Met His Phe Ala Leu Gln Arg Arg
 20 25 30
 Leu Pro Arg Thr Pro Pro Pro Ala Ser Arg Pro Ser Arg
 35 40 45

20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Thr Arg Trp Ser His Ser Trp Pro Gly Tyr Val Gly Gly Ala Asn
 1 5 10 15
 Pro Ser Pro Ala Thr Arg Pro Leu Pro Thr Arg Pro Ser Arg Thr Val
 20 25 30
 Glu Ser Cys
 35

30

35 (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 amin acids
 (B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

5 Ser Arg Tyr Asn Asp Leu Gly Thr Arg Pro Val Ser Glu Val Ile Lys
1 5 10 15
Tyr Asp Tyr Phe Pro Gly Tyr Ser Gln His Val Ile Thr Pro Asp Gly
20 25 30
Ser Tyr Ser Thr Arg Pro Leu Pro Ser Arg Pro Ser Arg Thr Val Glu
35 40 45
Ser Cys
10 50

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Pro Gly Arg Leu Leu Leu Pro Ser Glu Pro Arg Thr Phe Tyr Asn Tyr
1 5 10 15
Gly His Asp Ser Arg Pro Ser Arg
20 20

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Thr Met Tyr Gly Val Ser Trp Leu Ser Ser Gly Ser Gly Ile
1 5 10 15
Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg Pro Ser Arg
20 25 30

30

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Ser Ser Cys Thr Glu Lys Thr Val Ser Gly Trp Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Pr Leu Pr Ile Leu Pr Arg Thr Thr Arg Pro Ser Arg
 20 25 30

5 (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ser Ser Cys Met Leu Pro Thr Asp Gly Trp Gln Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Pro Arg Pro Leu Pro Met Leu Pro Thr Thr Arg Pro Ser Arg
 20 25 30

15 (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ser Ser Cys Asp Gly Thr Gln Phe Arg Leu Asn Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Asn Arg Pro Leu Pro Met Ile Pro Thr Thr Arg Pro Ser Arg
 20 25 30

25 (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Ser Cys Met Gln Gly Gln Ala Gly Leu Lys Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Pro Leu Pro Ser Leu Pro Ile Thr Thr Arg Pro Ser Arg
 20 25 30

35

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ser Ser Cys Tyr Arg Glu Lys Asp Thr Trp Gly Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Ser Arg Pro Leu Pro Ser Leu Pro Thr Thr Arg Pro Ser Arg
 20 25 30

10 (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ser Ser Cys Leu Phe Glu Gln Gly Ala Gly Thr Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Ser Leu Pro Pro Leu Pro Pro Thr Thr Arg Pro Ser Ser Arg
 20 25 30

20 (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser Ser Cys Asp Thr Gly Arg Ile Ala Pro Gly Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Pro Arg Pro Leu Pro Leu Ile Pro Thr Thr Pro Arg Ser Thr Asn
 20 25 30
 Leu Asn Leu Thr Ser Thr Thr Thr Arg Pro Ser Arg
 35 40

30

(2) INFORMATION FOR SEQ ID NO:60:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ser Ser Cys Gly Leu Asp Asn Ala Ala Lys Thr Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Pro Leu Pro Pro Thr Pro Leu Thr Thr Arg Pro Ser Arg
 20 25 30

5

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser Ser Cys Ser Arg Ala His Glu Thr Glu Met Cys Gly Ser Arg Ser
 1 5 10 15
 Thr Arg Pro Gln Pro Pro Pro Pro Ile Thr Thr Arg Pro Ser Arg
 20 25 30

15

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg Ser Thr Pro Arg Pro Leu Pro Met Leu Pro Thr Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:63:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:64:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:
- Val Leu Lys Arg Pro Leu Pro Ile Pro Pro Val Thr Arg
1 5 10
- 5 (2) INFORMATION FOR SEQ ID NO:65:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:
- Gly Pro His Arg Arg Leu Pro Pro Thr Pro Ala Thr Arg
1 5 10
- (2) INFORMATION FOR SEQ ID NO:66:
- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:
- 20 Ala Asn Pro Ser Pro Ala Thr Arg Pro Leu Pro Thr Arg
1 5 10
- (2) INFORMATION FOR SEQ ID NO:67:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- 25 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:
- 30 Arg Ser Thr Pro Arg Pro Leu Pro Pro Leu Pro Thr Thr Arg
1 5 10
- (2) INFORMATION FOR SEQ ID NO:68:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
- 35 (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Gly Thr Val 1u Pr Val Pro Pro Pro Val Pr Pro Arg Arg Arg Pr
 1 5 10 15
 1u Ser Ala

(2) INFORMATION FOR SEQ ID NO:69:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

10

Lys Ile Ser Pro Pro Thr Pro Lys Pro Arg Pro Pro Arg Pro Leu Pro
 1 5 10 15
 Val

(2) INFORMATION FOR SEQ ID NO:70:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

20

Leu Ala Pro Pro Lys Pro Pro Leu Pro Glu Gly Glu Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 2
 (D) OTHER INFORMATION: /note= "any residue other than Cys"

(ix) FEATURE:

30

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 5..6
 (D) OTHER INFORMATION: /note= "any hydrophobic residue"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Arg Xaa Leu Pro Xaa Xaa Pro
 1 5

35

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids

(B) TYPE: amin acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

5 Pro Gly Phe Arg Glu Leu Pro Pro Leu Pro Pro Ser Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala Gln Ser Arg Pro Leu Pro Ile Pro Pro Glu Thr Arg
1 5 10

15

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Pro Pro Asn Ser Pro Leu Pro Pro Leu Pro Thr His Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:75:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

30

Thr Gly Arg Gly Pro Leu Pro Pro Leu Pro Asn Asp Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Tyr Ser Thr Arg Pro Val Pr Pro Ile Thr Arg Pr Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:77:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

10

Ser His Lys Ser Arg Leu Pro Pro Leu Pro Thr Arg Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Tyr Arg Phe Arg Ala Leu Pro Ser Pro Pro Ser Ala Ser
1 5 10

20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Leu Ala Gln Arg Gln Leu Pro Pro Thr Pro Gly Arg Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:80:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

35

Ala Leu Gln Arg Arg Leu Pro Arg Thr Pr Pr Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Pro Ala Thr Arg Pro Leu Pro Thr Arg Pro Ser Arg Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:82:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

15 Tyr Ser Thr Arg Pro Leu Pro Ser Arg Pro Ser Arg Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:83:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

25 Xaa Pro Gly Arg Ile Leu Leu Leu Pro Ser Glu Pro Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ser Gly Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn
 1 5 10

35 (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

5 Arg Ser Thr Arg Pro Leu Pro Ile Leu Pro Arg Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ser Thr Pro Arg Pro Leu Pro Met Leu Pro Thr Thr Arg
1 5 10

15

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ser Thr Asn Arg Pro Leu Pro Met Ile Pro Thr Thr Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:88:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

30

Arg Ser Thr Arg Pro Leu Pro Ser Leu Pro Ile Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Ser Thr Ser Arg Pro Leu Pr Ser Leu Pr Thr Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:90:

5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

10

Arg Ser Thr Arg Pro Leu Pro Ser Leu Pro Ile Thr Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:91:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

20

Arg Ser Thr Arg Gln Leu Pro Ile Pro Pro Thr Thr Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:92:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

30

Ser Thr Pro Arg Pro Leu Pro Leu Ile Pro Thr Thr Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Arg Ser Thr Arg Pro Leu Pr Pr Thr Pr Leu Thr Thr

1

5

10

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Arg Ser Thr Arg Pro Gln Pro Pro Pro Pro Ile Thr Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Arg Pro Leu Pro Met Leu Pro
1 5

20 (2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "Pro or Met"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Arg Pro Leu Pro Xaa Leu Pro
1 5

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Arg Ser Thr Pr
1

(2) INFORMATION FOR SEQ ID NO:98:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

10 Arg Ser Thr Pro Ala Pro Pro Val Pro Pro Arg Thr Thr Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:99:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AGCGTAACGA TCTCCCG

17

(2) INFORMATION FOR SEQ ID NO:100:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear
 25 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TTCACCTCGA AAGCAAGCTG

20

(2) INFORMATION FOR SEQ ID NO:101:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CCTCATAGTT AGCGTAACG

19

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

AGCGTAACGA TCTAAA

16

10 (2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Lys Ser Gly Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:104:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

25 Gly Ser Gly Ser
1

(2) INFORMATION FOR SEQ ID NO:105:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

35 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

5

Ser Ser Cys Asp His Thr Leu Gly Leu Gly Trp Cys Gly Ser Arg Ser
1 5 10 15

Thr Arg Gln Leu Pro Ile Pro Pro Thr Thr Thr Arg Pro Ser Arg
20 25 30

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WHAT IS CLAIMED IS:

1. A peptide having at least nine and up to forty-five amino acid residues, including an amino acid sequence of the formula, R-2-L-P-5-6-P-8-9 (SEQ ID NO:10), positioned
5 anywhere along the peptide, in which each number represents an amino acid residue, such that 2 represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, 8 represents any amino acid residue except cysteine, and 9 represents a hydrophilic amino
10 acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src, provided that said peptide is not R-P-L-P-P-L-P-T-S (SEQ ID NO:11).
- 15 2. The peptide of claim 1 in which 2 is a P, R, A, L, Q, E or S.
3. The peptide of claim 1 in which 5 is a P, M, I or L.
4. The peptide of claim 1 in which 6 is a P, L, I or
20 V.
5. The peptide of claim 1 in which 8 is a T, R, P, I, N, E, V, S, A, G or L.
6. The peptide of claim 1 in which 9 is a T, R, S, H or D.
- 25 7. The peptide of claim 1 which further comprises a C-terminal-flanking amino acid sequence of the formula 10, 10-11, 10-11-12, 10-11-12-13 (SEQ ID NO:12) or 10-11-12-13-14 (SEQ ID NO:13), in which each number represents any amino acid residue except cysteine, such that 10 is bound to 9 by a
30 peptide bond.
8. The peptide of claim 7 in which 10 is T, R, L, S, D, P, A or N.
9. The peptide of claim 7 in which 11 is R, P, A, Q, S or T.
- 35 10. The peptide of claim 7 in which 12 is P, S, R or T.
11. The peptide of claim 7 in which 13 is P, S, R, F, H or T.

12. The peptide of claim 7 in which 14 is S, R, G or T.
13. The peptide of claim 1 which further comprises an N-terminal-flanking amino acid sequence of the formula 1', 2'-1', 3'-2'-1' or 4'-3'-2'-1' (SEQ ID NO:14) in which each number represents any amino acid residue except cysteine, such that 1' is bound to R by a peptide bond.
14. The peptide of claim 13 in which 1' is T, P, S, N, F, W, K, H, Q or G.
15. The peptide of claim 13 in which 2' is S, T, G, P, R, Q, L, A or H.
16. The peptide of claim 13 in which 3' is R, S, P, G, A, V, Y or L.
17. The peptide of claim 13 in which 4' is R, S, V, T, G, L or F.
18. A peptide having at least thirteen and up to forty-five amino acid residues, including an amino acid sequence of the formula, 3'-2'-1'-R-2-L-P-5-6-P-8-9-10 (SEQ ID NO:15), positioned anywhere along the peptide, in which each number represents an amino acid residue, such that 3', 2', 1', 2, 8, and 10 each represents any amino acid residue except cysteine, 5 and 6 each represents a hydrophobic amino acid residue, and 9 represents a hydrophilic amino acid residue except cysteine, each letter being the standard one-letter symbol for the corresponding amino acid, said peptide exhibiting a binding affinity for the SH3 domain of Src.
19. The peptide of claim 18 in which 5 is a P or M.
20. The peptide of claim 18 in which 1' is T, P, S or N.
21. The peptide of claim 18 in which 2' is S or T.
22. The peptide of claim 18 in which 3' is R or S.
23. The peptide of claim 18 in which 10 is T or R.
24. The peptide of claim 1 the binding affinity of which is at least three-fold greater than that exhibited by the peptide RPLPPLP for the SH3 domain of Src.
25. The peptide of claim 18 the binding affinity of which is at least three-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9) for the SH3 domain of Src.

26. The peptide of claim 1 with binding affinity which is at least four-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9) for the SH3 domain of Src.

27. The peptide of claim 18 with the binding affinity of 5 which is at least four-fold greater than that exhibited by the peptide RPLPPLP (SEQ ID NO:9) for the SH3 domain of Src.

28. The peptide of claim 1 which further exhibits a general binding affinity for the SH3 domain of Abl, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, p85 PI-3'Kinase, and proteins 10 related thereto.

29. The peptide of claim 1 which exhibits a selective binding affinity for the SH3 domain of Src and Src-related proteins.

30. The peptide of claim 18 which further exhibits a 15 general binding affinity for the SH3 domain of Abl, Grb2, PLC- δ , PLC- γ , Ras GAP, Nck, p85 PI-3'Kinase, and proteins related thereto.

31. The peptide of claim 18 which exhibits a selective binding affinity for the SH3 domain of Src and Src-related 20 proteins.

32. A peptide having the amino acid sequence RSTPRPLPMLPTTR (SEQ ID NO:62).

33. A peptide having the amino acid sequence RSTPRPLPPLPTTR (SEQ ID NO:67).

25 34. A peptide having the amino acid sequence GILAPPVPPRNTR (SEQ ID NO:63).

35. A peptide having the amino acid sequence VLKRPLPIPPVTR (SEQ ID NO:64).

36. A peptide having the amino acid sequence 30 GPHRRLPPTPATR (SEQ ID NO:65).

37. A peptide having the amino acid sequence ANPSPATRPLPTR (SEQ ID NO:66).

38. A peptide having an amino acid sequence selected from the group consisting of RSTRPLPILPRTT, STPRPLPMLPTTR, 35 STNRPLPMIPTTR, RSTRPLPSLPITT, STSRPLPSLPPTTR, RSTRSLPPLPPTT, RSTRQLPIPPPTT, STPRPLPLIPTTP, RSTRPLPPTPLTT, and RSTRPQPPPPITT (SEQ ID NOS:85-94).

39. A peptid having the amino acid s quenc selected from the group consisting of VLKRPLPIPPVTR (SEQ ID NO:64), YSTRPVPPITRPS (SEQ ID NO:76), SHKSRLPPLPTRP (SEQ ID NO:77), GPHRRLPPTPATR (SEQ ID NO:65), PATRPLPTRPSRT (SEQ ID NO:81), 5 and SGGILAPPVPPRN (SEQ ID NO:84).

40. A peptide having the amino acid sequence selected from the group consisting of PPNSPLPPLPTH (SEQ ID NO:72), TGRGPLPPLPND (SEQ ID NO:74), YRFRALPSPPSAS, LAQRQLPPTPGRD ALQRRLPRTPPPA (SEQ ID NOS:78-80), YSTRPLPSRPSRT, and 10 XPGRILLLPSEPR (SEQ ID NOS:82-83).

41. A construct comprising a nucleic acid encoding a peptide of claim 1 or its complement.

42. The construct of claim 41 which is a DNA polynucleotide.

15 43. The construct of claim 41 which is a RNA polynucleotide.

44. A construct comprising a nucleic acid encoding a peptide of claim 18 or its complement.

45. The construct of claim 44 which is a DNA 20 polynucleotide.

46. The construct of claim 44 which is a RNA polynucleotide.

47. The construct of claim 41 which is a transforming vector.

25 48. The construct of claim 44 which is a transforming vector.

49. A host cell transformed with the vector of claim 47.

50. A host cell transformed with the vector of claim 30 48.

51. A conjugate comprising a peptide of claim 1 and a second molecule.

52. The conjugate of claim 51 in which said second molecule is selected from the group consisting of an amino 35 acid, a peptide, a protein, a nucl ic acid, a nucl oside, a glycidic r sidu , a label, a drug r a small molecule.

53. A diagnostic kit for the detection of SH3 domains comprising an SH3 domain-binding peptide and a detectable label conjugated to said peptide directly, indirectly or by complexation, said peptide comprising: (i) a core sequence motif of the formula RXLP $\phi\phi$ P (SEQ ID NO:71), wherein X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue, each letter representing the standard one-letter designation for the corresponding amino acid residue; and (ii) two or more additional amino acid residues flanking said core sequence at its C-terminal end, N-terminal end or both.

54. A drug delivery system comprising an SH3 domain-binding peptide and a drug conjugated to said peptide directly, indirectly or by complexation, said peptide comprising: (i) a core sequence motif of the formula RXLP $\phi\phi$ P (SEQ ID NO:71), wherein X represents any amino acid except cysteine and ϕ represents a hydrophobic amino acid residue, each letter representing the standard one-letter designation for the corresponding amino acid residue; and (ii) two or more additional amino acid residues flanking said core sequence at its C-terminal end, N-terminal end or both.

55. The drug delivery system of claim 54 which may be administered parenterally, orally, enterally, topically or by inhalation.

56. The drug delivery system of claim 54 which may be administered intranasally, ophthalmically or intravaginally.

57. The drug delivery system of claim 54 which is in the form of a solid, gel, liquid or aerosol.

58. A method of modulating the activity of Src or Src-related proteins comprising administering a composition comprising an effective amount of a peptide of claim 1 and a carrier.

59. The method of claim 58 which inhibits the activity of Src or Src-related proteins.

60. The method of claim 58 which activates Src or Src-related proteins.

61. A method of identifying a peptide having a region that binds to an SH3 domain comprising:

- (a) providing an immobilized target protein comprising an SH3 domain;
- 5 (b) incubating said immobilized target protein with an aliquot taken from a random peptide library;
- (c) washing unbound peptide from said immobilized target protein;
- (d) recovering the peptide bound to said
- 10 immobilized target protein; and
- (e) determining the primary sequence of the SH3 domain-binding peptide.

62. The method of claim 61 in which said library is a displayed random peptide library.

15 63. The method of claim 62 in which said library is a phage-displayed random peptide library.

64. The method of claim 62 in which said library is a phagemid-displayed random peptide library.

65. The method of claim 61 in which step (c) includes

20 washing unbound phage from said immobilized target protein; step (d) includes recovering the phage bound to said immobilized target protein; and step (e) includes determining the relevant nucleotide sequence of said binding phage nucleic acid, from which the primary sequence corresponding

25 to the SH3 domain-binding peptide is deduced.

66. A method of identifying a peptide having a region that binds to an SH3 domain comprising:

- (a) providing an immobilized target protein comprising an SH3 domain;
- 30 (b) incubating said immobilized target protein with an aliquot taken from a phage-displayed random peptide library, which library includes peptides having a random sequence of ≥ 8 amino acid residues;
- (c) washing unbound phage from said immobilized
- 35 target protein;
- (d) recovering the phage bound to said immobilized target protein; and

(e) determining the relevant nucleotide sequence of said binding phage nucleic acid and deducing the primary sequence corresponding to the SH3 domain-binding peptide.

67. The method of claim 66 which further comprises amplifying the titer of the recovered phage.

68. The method of claim 66 which further comprises repeating the steps of incubation, washing and recovery to provide SH3 domain-binding peptide-enriched phage.

69. A pharmaceutical composition comprising an SH3 domain-binding peptide and a pharmaceutically acceptable carrier, said peptide comprising: (i) a 9-mer sequence motif of the formula RXLP ϕ ϕ PX ψ (SEQ ID NO:10), wherein X represents any amino acid except cysteine, ϕ represents a hydrophobic amino acid residue, and wherein ψ is a hydrophilic amino acid residue except cysteine, each letter representing the standard one-letter designation for the corresponding amino acid residue; and, optionally, (ii) additional amino acid residues flanking said 9-mer sequence at its C-terminal end, N-terminal end or both, up to a total of 45 amino acid residues, including said 9-mer sequence.

70. The composition of claim 69 in which at least one additional amino acid flanks said 9-mer sequence.

71. The composition of claim 69 in which at least two additional amino acids flank said 9-mer sequence.

72. The composition of claim 69 in which at least three additional amino acids flank said 9-mer sequence.

73. A method of disrupting protein tyrosine kinase-mediated signal transduction pathways comprising administering an effective amount of a peptide of claim 1.

74. A method of regulating the processing, trafficking or translation of RNA by administering an effective amount of a peptide of claim 1.

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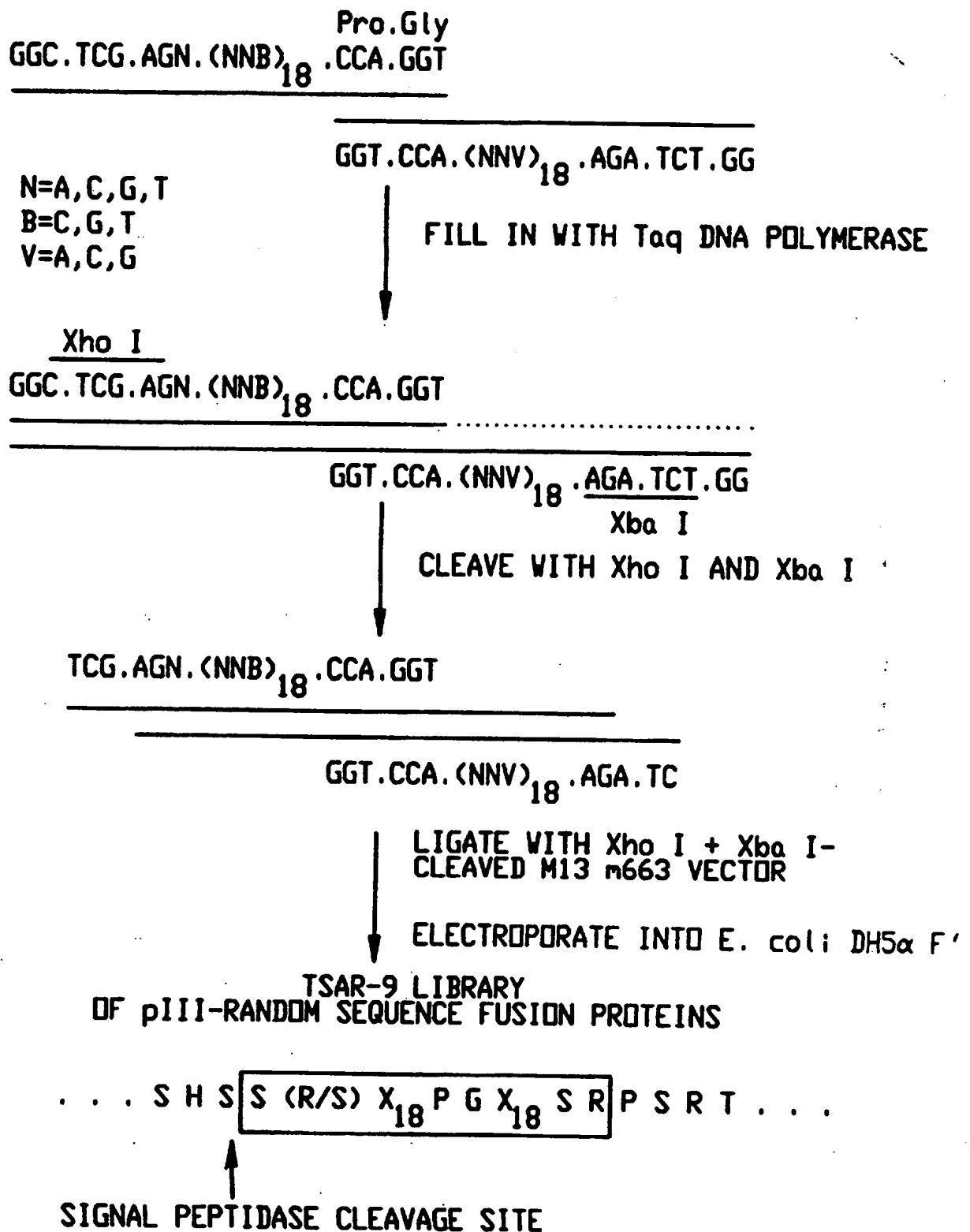


FIG.1

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Gly

tt.ttg.tcg.acN.(NNB)₁₀.Ngc.ggt.g

N=A,G,T,C
B=G,T,C
V=G,A,C

cg.cca.cNV.(NNV)₁₀.tga.tca.ttt.t

FILL IN WITH Taq DNA POLYMERASE

Sal I

tt.ttg.tcg.acN.(NNB)₁₀.Ngc.ggt.g

cg.cca.cNV.(NNV)₁₀.tga.tca.ttt.t
Spe I

CLEAVE WITH Sal I + Spe I

tcg.acN.(NNB)₁₀.Ngc.ggt.g

cg.cca.cNV.(NNV)₁₀.tga.tc

LIGATE WITH Xho I + Xba I -
CLEAVED M13 m663 VECTOR

ELECTROPORATE INTO E. coli DH5α F'

TSAR-12 LIBRARY
OF pIII-RANDOM SEQUENCE FUSION PROTEINS

... S H S S (S/T) X₁₀ Φ G θ X₁₀ T R P S R T ...

Φ=S,R,G,C, OR W

θ=V,A,D,E, OR G

SIGNAL PEPTIDASE CLEAVAGE SITE

FIG.2

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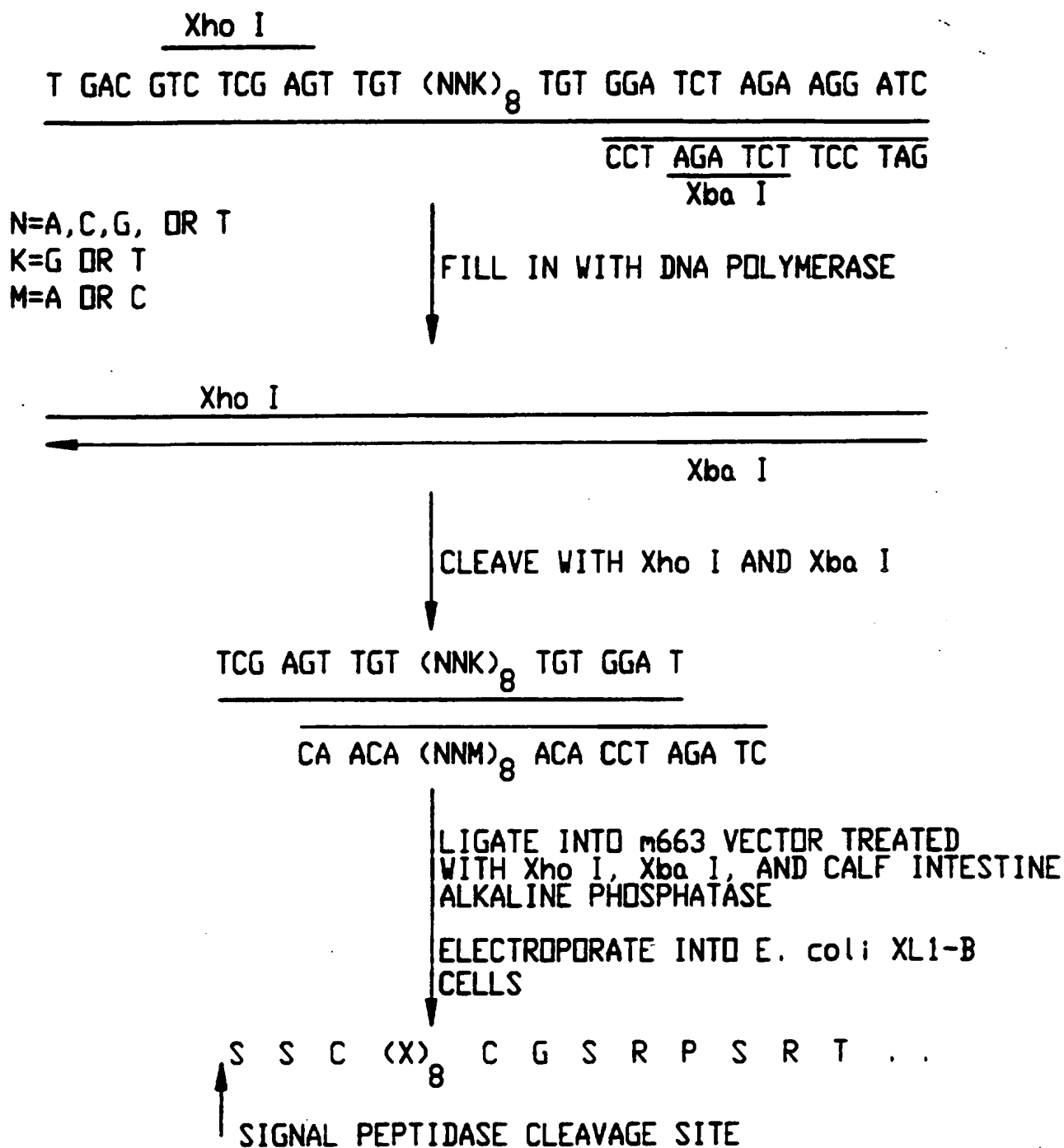


FIG.3

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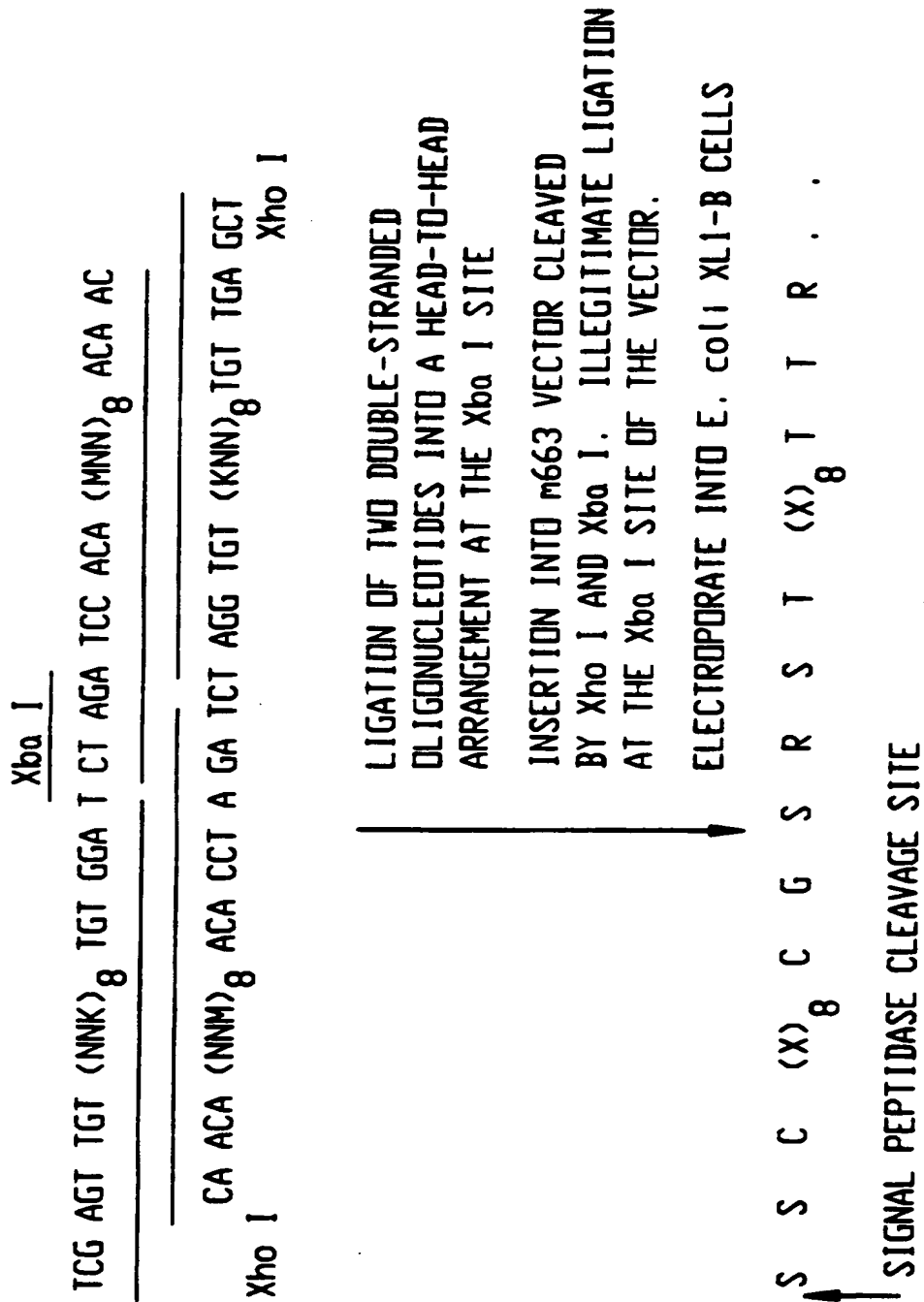


FIG.4

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[illegible]

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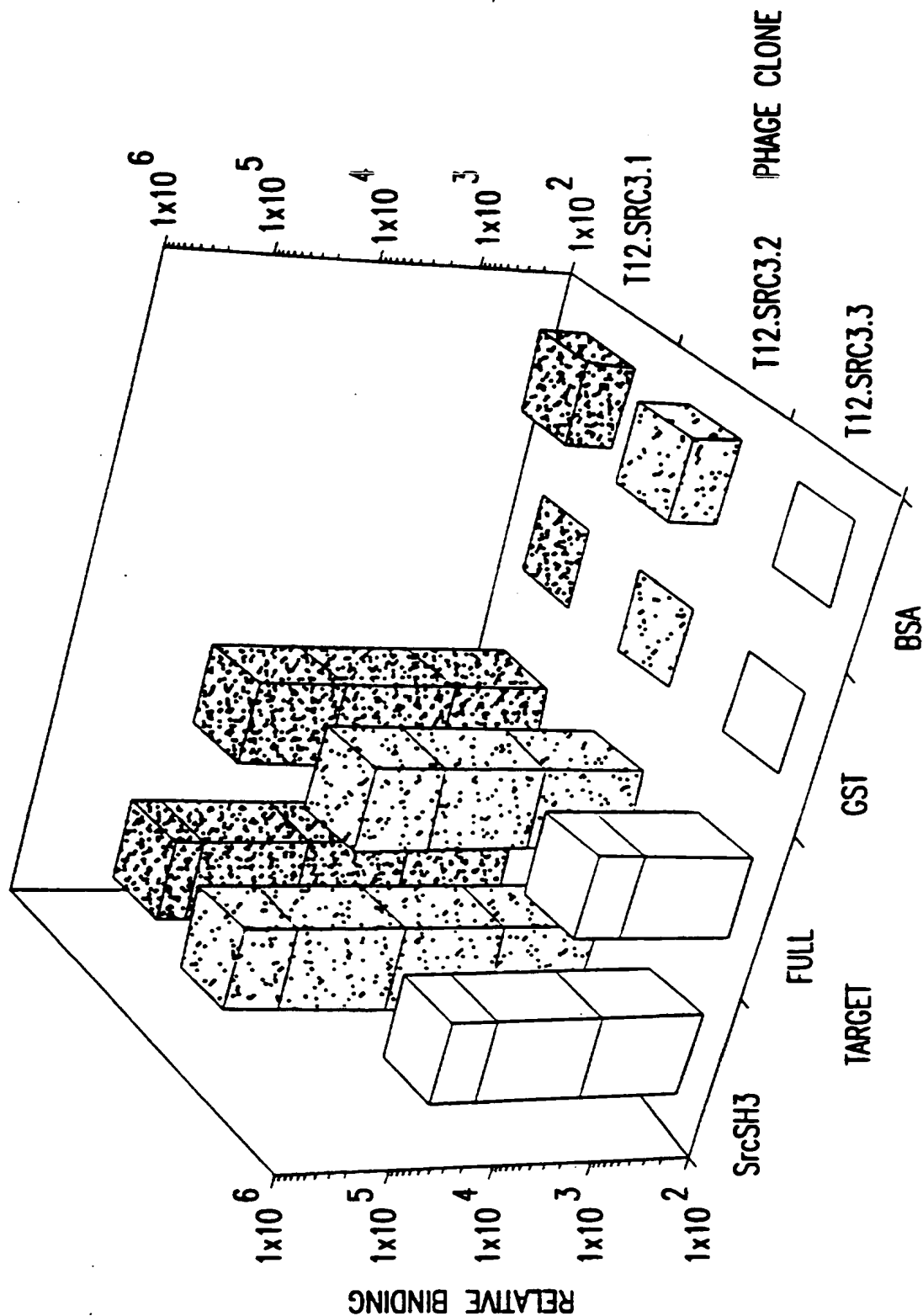


FIG.6

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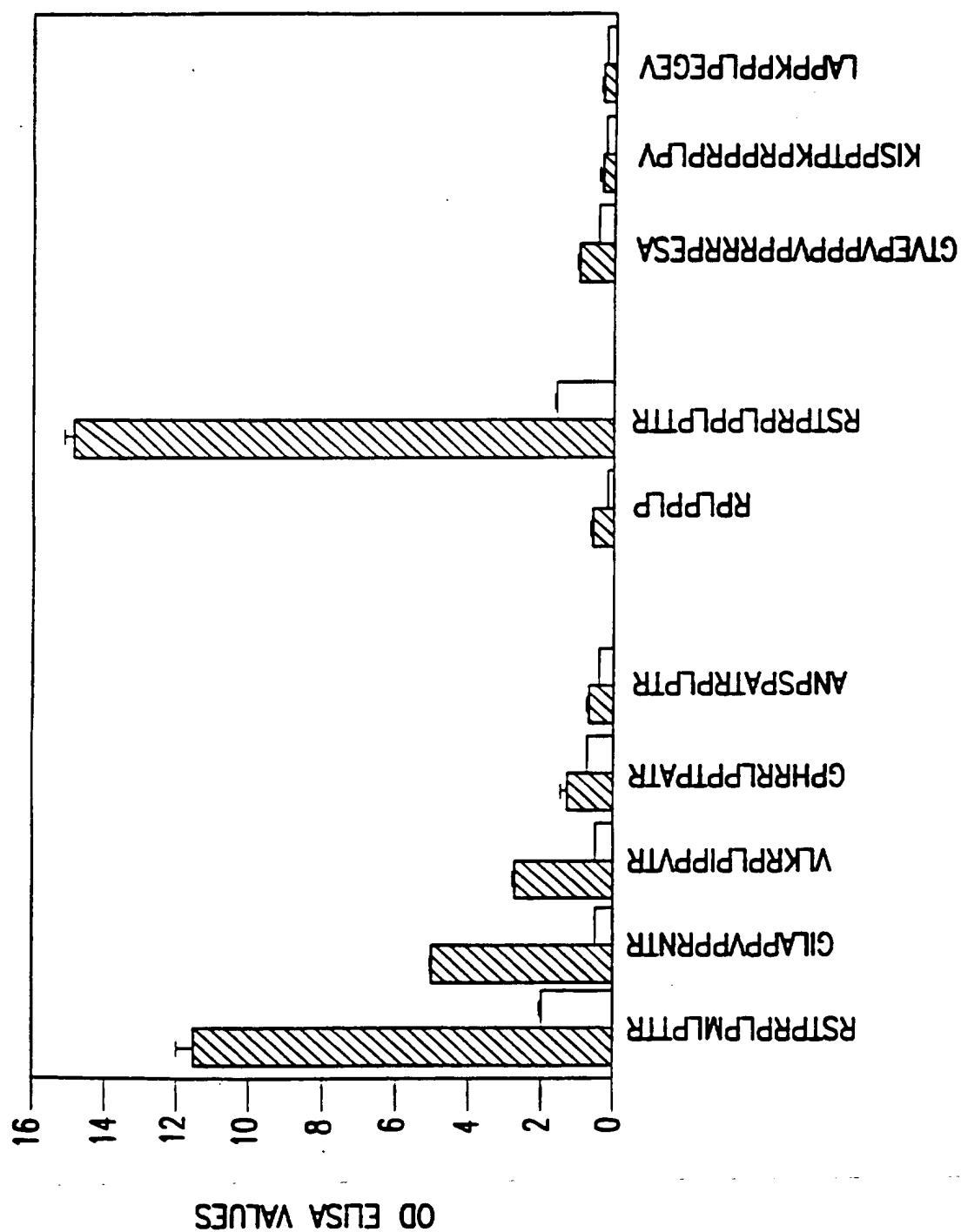


FIG. 7

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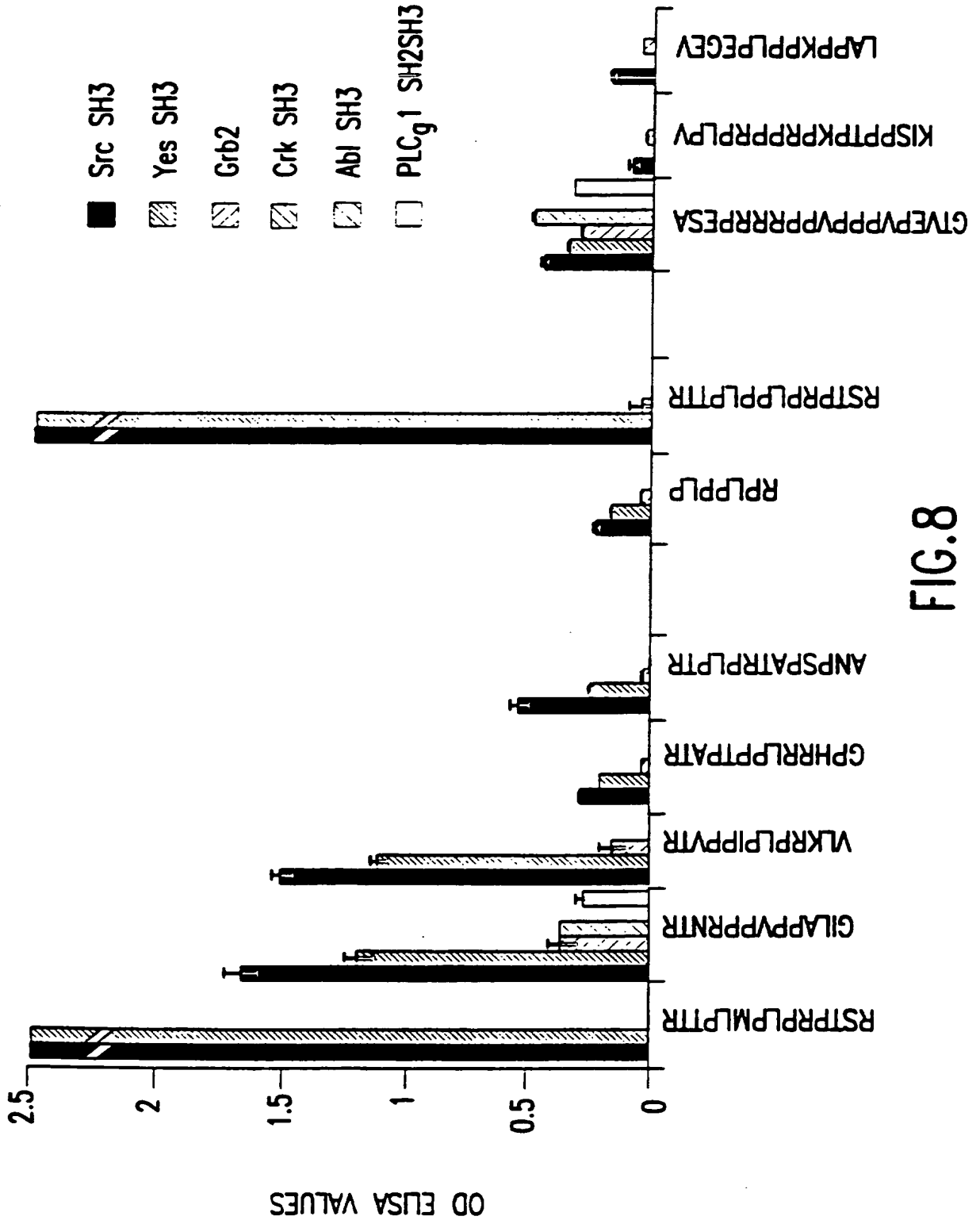


FIG. 8

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PEPTIDES:
(MICROMOLAR
CONCENTRATION)

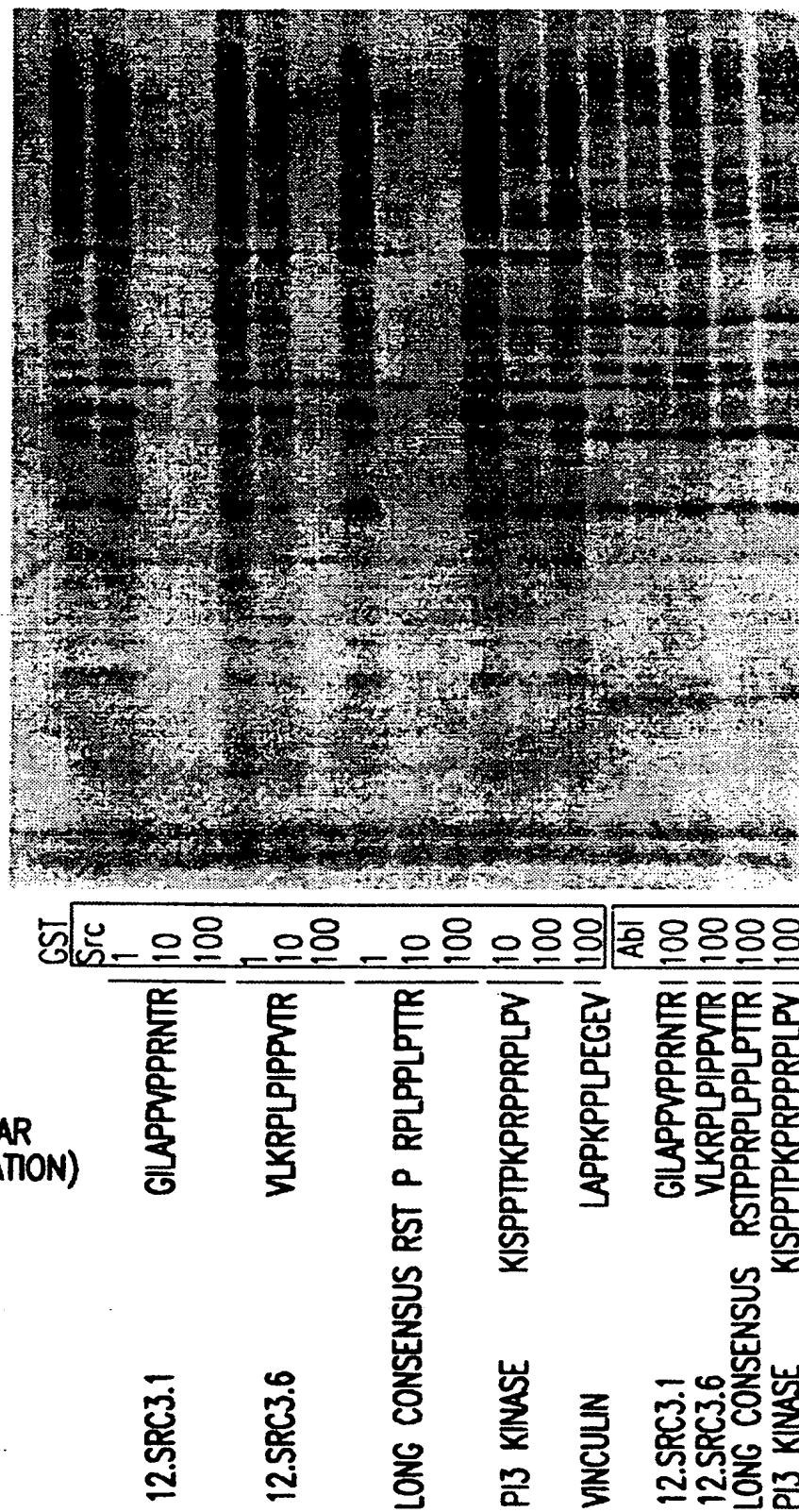


FIG.9

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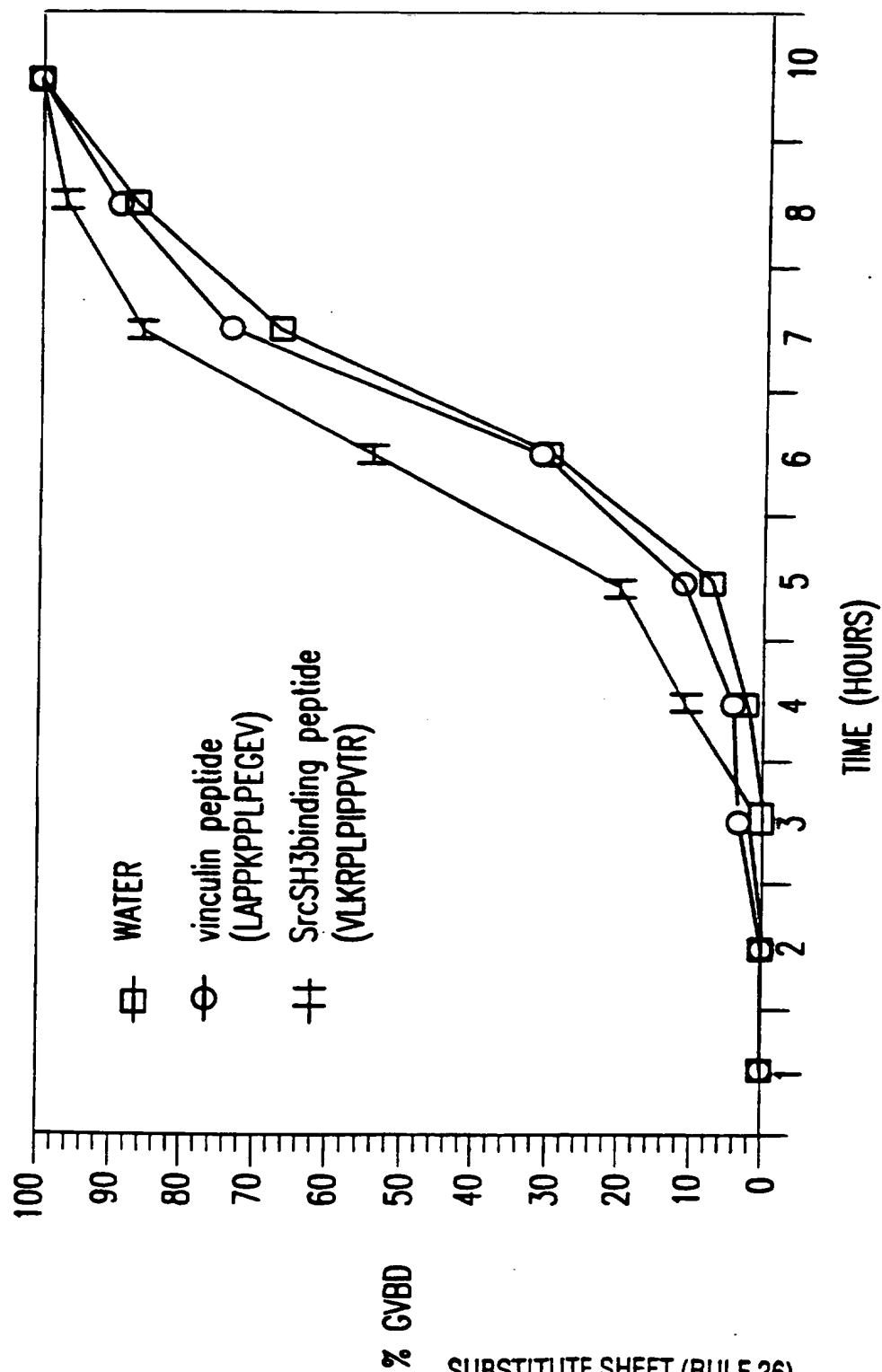


FIG.10

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FIG. 11A

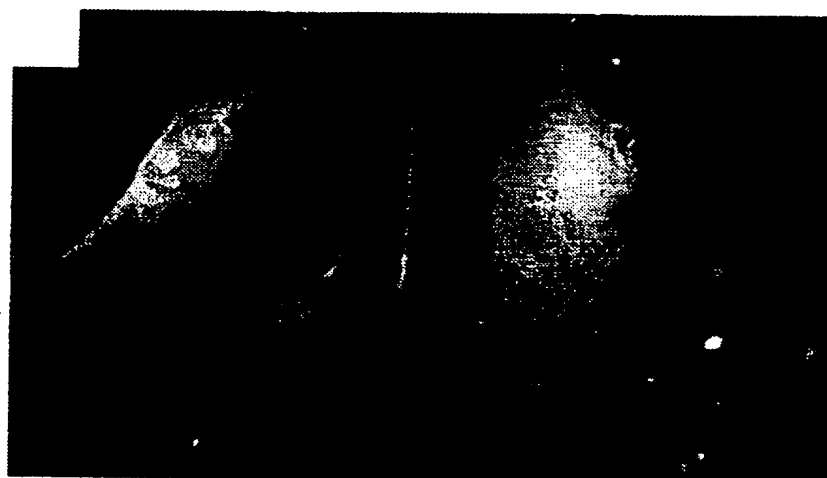


FIG. 11B

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FIG. 11C

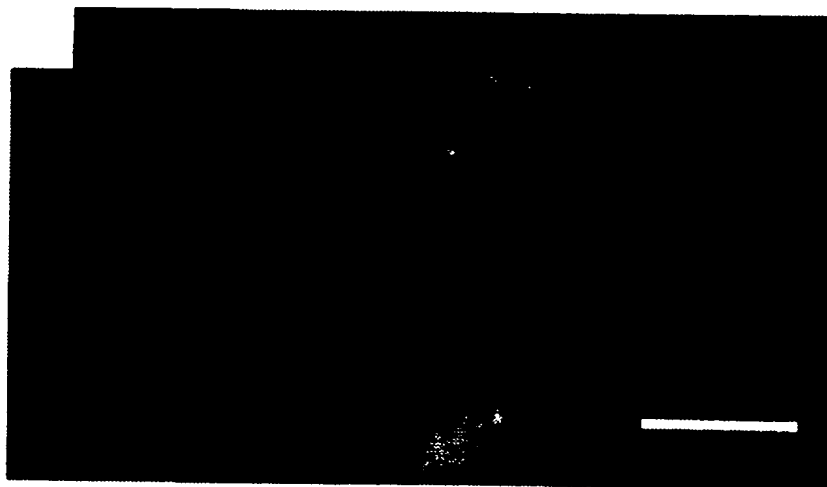


FIG. 11D

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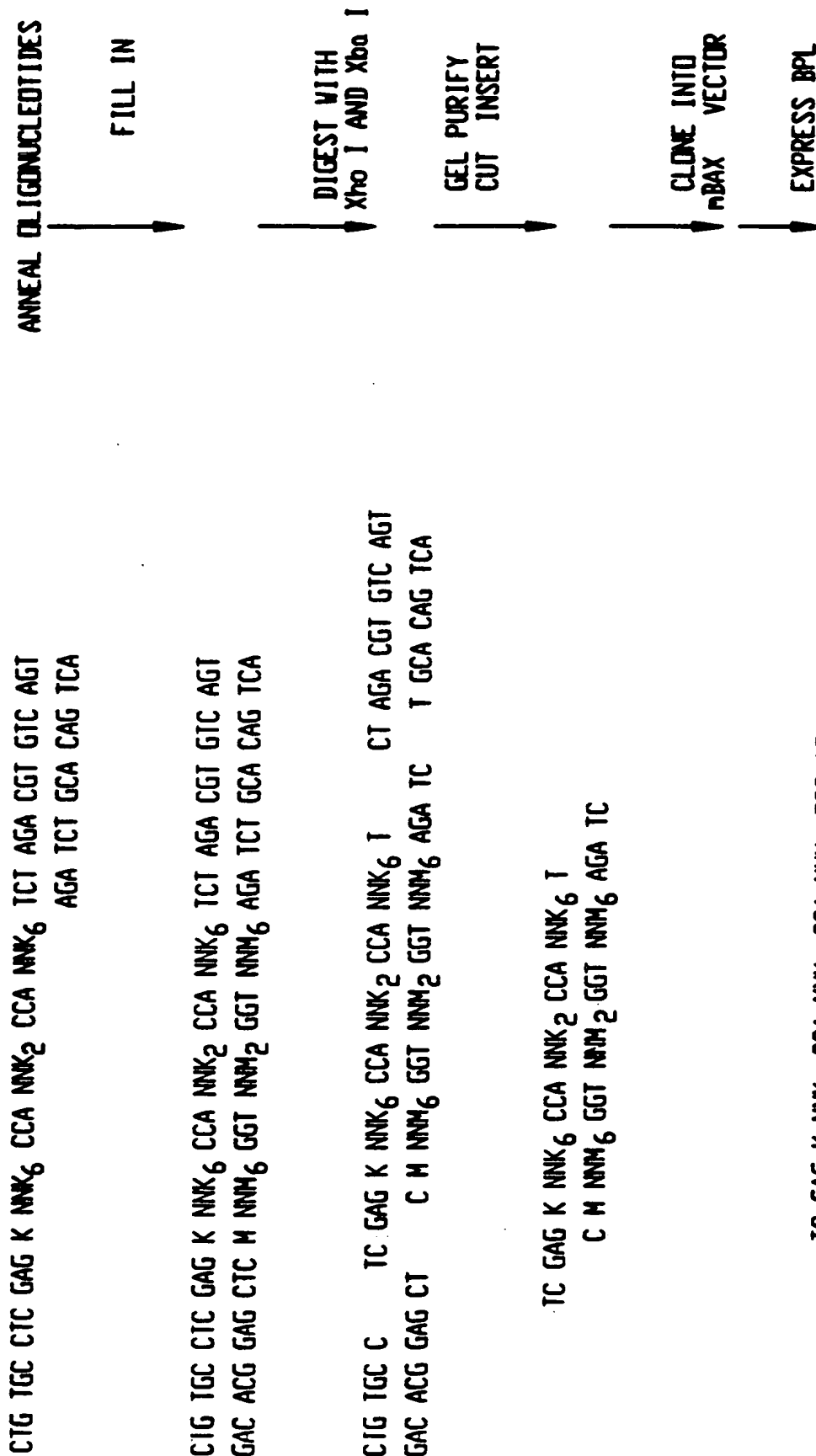


FIG.12

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mBAX

SIGNAL PEPTIDE
 CLEAVAGE SITE

-1 ↓ +1

S S I D M P T A S T M Y N M L H R N E P
 . . TCCTCGAGTATCGACATGCCCTTAGACTGCTAGCACTATGTACACATGCTTCATCGCAACGAGCCA
 Xho I

. . . epitope, mAb . . .

G G R K L S P P A N D M P P A L L K R S R
 GGTGGAGGAAGTTGAGCCCGCCGCAACGACATGCCGCCGCCCTCCTGAAGAGGTCTAGA . .
 Xba I

FIG.13

SUBSTITUTE SHEET (RULE 26)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/09382

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : 435/5, 7.1, 172.1, 320.1; 530/300; 514/2

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/5, 7.1, 172.1, 320.1; 530/300; 514/2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG, STN

search terms: sh3, src, peptides

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X, P	The Journal of Biological Chemistry, Volume 269, Number 39, issued 30 September 1994, Sparks et al., "Identification and Characterization of Src SH3 Ligands from Phage-displayed Random Peptide Libraries", pages 23853-23856, see entire article.	1-74
X --- Y	Journal of the American Chemical Society, Volume 115, issued 1993, Chen et al. "Biased Combinatorial Libraries: Novel Ligands for the SH3 Domain of Phosphatidylinositol 3-Kinase", pages 12591-12592, see entire article, especially Tables I and II.	1-6, 24, 26, 28, 29, 53 ----- 7-23, 25, 27, 30-51, 53-74

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

•	Special categories of cited documents:	T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
•A	document defining the general state of the art which is not considered to be part of particular relevance		
•E	earlier document published on or after the international filing date	•X	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
•L	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	•Y	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
•O	document referring to an oral disclosure, use, exhibition or other means		
•P	document published prior to the international filing date but later than the priority date claimed	•A	document member of the same patent family

Date of the actual completion of the international search 19 OCTOBER 1995	Date of mailing of the international search report 01 NOV 1995
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile N . (703) 305-3230	Authorized officer <i>Lora M. Green</i> LORA M. GREEN Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/09382

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Science, Volume 249, issued 28 September 1990, Langer, "New Methods of Drug Discovery", pages 1527-1533, see entire article.	51, 52, 54-57
Y	Science, Volume 257, issued 07 August 1992, Cicchetti et al., "Identification of a Protein That Binds to the SH3 Region of Abl and Is Similar to BCR and GAP-rho"; pages 803-806, see entire article.	7-23, 25, 27, 30-50
Y	Gene, Volume 128, issued 1993, Kay et al., "An M13 Phage Library Displaying Random 38-amino-acid Peptides as a Source of Novel Sequences with Affinity to Selected Targets", pages 59-65, see entire article.	7-23, 25, 27, 30-48, 61-68

Form PCT/ISA/210 (continuation of second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/09382

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

G01N 33/53; C12Q 1/70; C12N 5/10. 7/01; C07K 7/00, 14/00; A61K 38/03

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